RAYSTATION 9A

RayPhysics Manual

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Disclaimer

For information on functionality not available for regulatory reasons, see the Regulatory Information in the Instructions for Use.

Safety notices

This user documentation contains WARNINGS concerning the safe use of the product. These must be followed.

WARNING!

The general warning sign informs you of a risk for bodily harm. In most cases the risk is related to mistreatment of the patient.

Note: *The note informs of a risk for loss of data or other impairment of the work.*

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1 INTRODUCTION

About this manual

This manual describes the RayPhysics application for LINACs, Ion treatment machines and NCT treatment machines. The algorithms and beam model parameters are described in more detail the *RSL-D-RS-9A-RCF, RayStation 9A Reference Manual*.

For LINACs: The RayPhysics application allows input of LINAC geometry and LINAC/R&V-constraints and creation of a beam model for dose computation. It is also possible to import QA phantoms and setup CT-lookup tables.

For Ion treatment machines: In RayPhysics it is possible to view and edit a majority of the machine parameters for all machines in the machine database. For PBS machines it is also possible to import and export measurements, perform auto-modeling of the machine, compute dose and compare to measurements. The final commissioning of the machine can only be performed by RaySearch staff. The uncommissioned machine with all measurements and relevant machine parameters should be saved as an rsbak-file and sent to support@raysearchlabs.com for final commissioning.

In this chapter

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1.1 THE RAYPHYSICS APPLICATION

The RayPhysics application contains three modules. All modules are described in this document.

- The **Beam Commissioning** module is used for virtual treatment machine definition.
- The **Beam 3D Modeling** module is used to specify a phantom for QA measurements and to test dose computation on arbitrary plans also with uncommissioned machines.
- The **CT Commissioning** module is used to specify the interpretation of CT-data from different CTs.

1.2 STARTING RAYPHYSICS

The RayStation Launcher application handles startup of the following applications: RayStation, RayPhysics and RayBiology. The startup icons will reflect the available licenses.

The manuals and any applicable field safety notice documents are available by clicking the **RayDocumentation** icon.

Click the RayPhysics icon in the RayStation Launcher application to start the RayPhysics application.

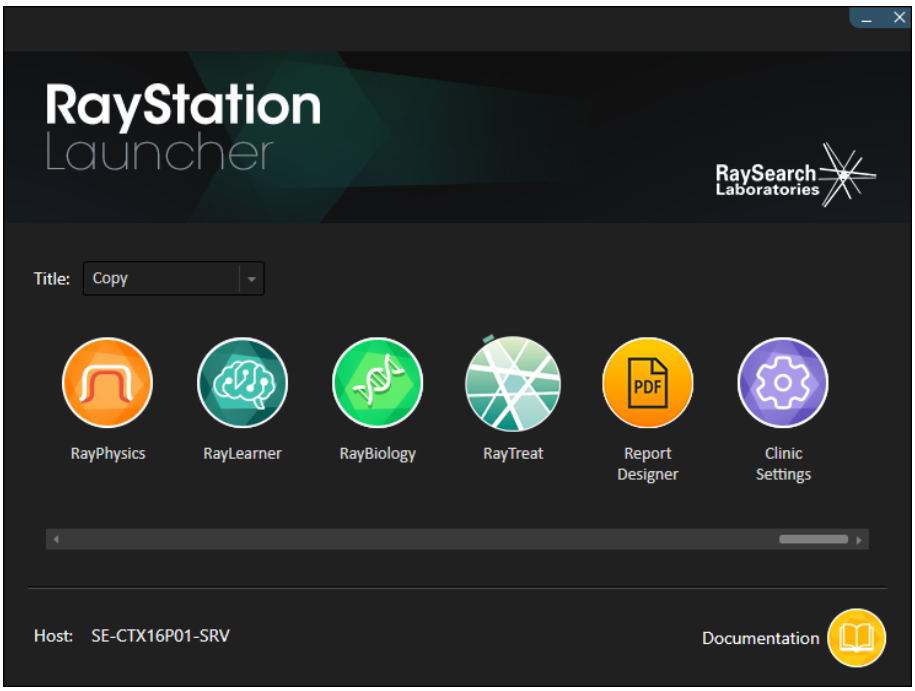
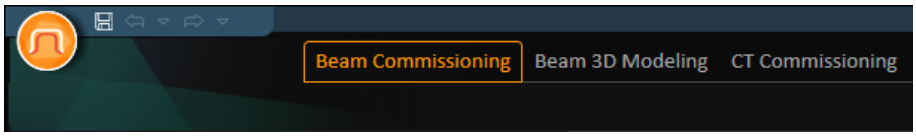


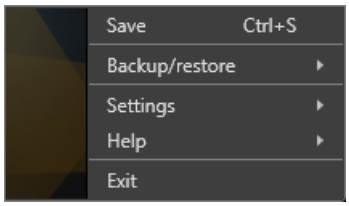
Figure 1. The RayStation Launcher application.

1.3 USER INTERFACE TOP BAR

The top bar contains, from left to right, the RayPhysics drop-down menu (below the orange icon), Save all to database (the diskette icon), undo and redo with drop-down menus.



The drop-down menu in the orange icon gives access to save, support backup and restore, GPU settings, help and exit. Note that any save to database (including commission and deprecate autosave) clears the undo/redo stack.



1.4 GPU SETTINGS - SELECT GPUS TO USE FOR COMPUTATIONS

Computations of Collapsed Cone photon dose, Carbon ion Pencil Beam dose and deformable registrations are done using GPU (graphics processing unit). Selection of which GPUs to use for accelerated computations, and validations of system environment for GPU computations, is reached from the **Settings** menu in the RayStation or RayPhysics menu.

This opens the **Select GPUs to use for computations** dialog.

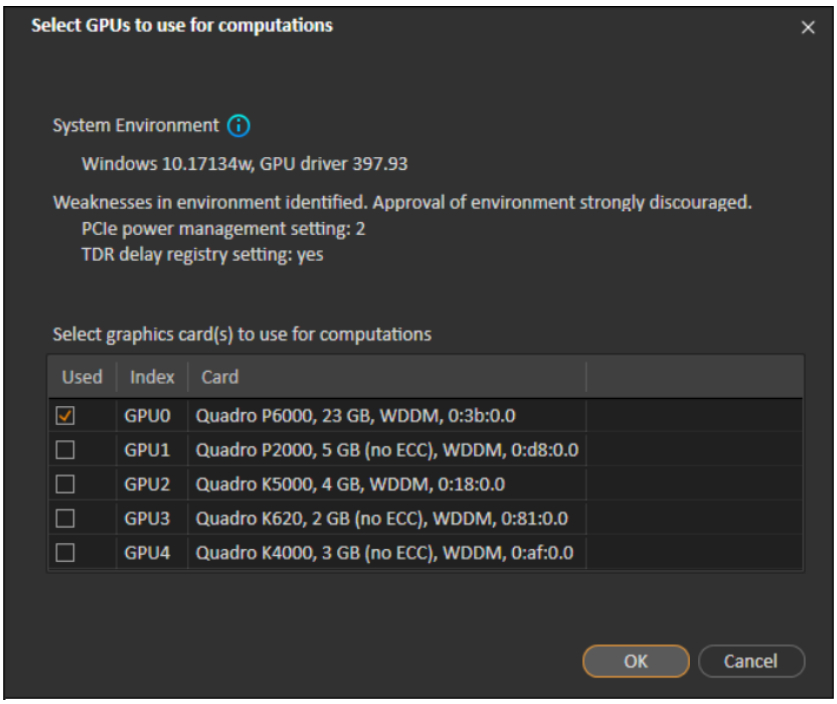


Figure 2. The Select GPUs to use for computations dialog.

When the **Select GPUs to use for computations** dialog is opened, RayStation or RayPhysics will scan the computer and list all GPUs found with number, name and other information. Not all GPUs listed may be supported for computations. System information and, if applicable, some types of system weaknesses are also displayed.

Note: *The GPU model affects the computational result Due to minor differences in hardware design, floating-point arithmetic imprecisions lead to clinically insignificant computational differences.*

1.4.1 System environment

Ensure that the selected cards, OS and driver versions are listed as valid combinations in the *RSL-D-RS-9A-SEG, RayStation 9A System Environment Guidelines*.

Before clinical use, verify operation of GPU computations using the *RSL-D-RS-9A-SEAT, RayStation 9A System Environment Acceptance Test Protocol*. RayStation will monitor the parameters displayed in the dialog. If changes are identified, GPU computations will not be possible.

Note that GPU computations may be affected by other environment parameters than those monitored by RayStation. All changes to the computer environment must be verified using the *RSL-D-RS-9A-SEAT, RayStation 9A System Environment Acceptance Test Protocol*.

1.4.2 Environment weaknesses

Some controls of weaknesses in the environment are run. If weaknesses are found they are presented in a separate section. Approval of an environment with identified weaknesses is strongly discouraged.

Computations on the GPU are sensitive to the Windows Timeout Detection and Recovery (TDR) mechanism. If a sub-computation on the GPU runs longer than about 2 seconds this mechanism may, by design, result in a program crash. The carbon dose optimization and computation has been verified to pass the TDR mechanism for complex cases with, e.g., 200 000 spots, 4 beams, target volume 5 dm^3 and voxels size of 0.2 x 0.2 x 0.2 cm^3 on validated GPUs.

If the GPU that is selected in the dialog is listed as "ECC off", the ECC RAM must be enabled in the GPU driver settings. "No ECC" is displayed if the GPU does not have any ECC RAM.

WARNING!

Use of non-ECC GPU memory. GPUs used for computations must have ECC RAM and the ECC state must be enabled in the GPU driver settings. Photon CC dose and deformable image registration may however be computed on GPUs without ECC RAM. (115893)

1.4.3 Hardware environment self test

To prevent RayStation or RayPhysics to run in a faulty hardware environment, a self test is run when launching RayStation or RayPhysics. The test consists of dose computations and deformable registration calculations compared with predefined results.

If the test fails the user is notified and no GPU computations will be possible.

The test will also be run for all selected GPUs to use for accelerated computations

WARNING!

Dose calculation on GPU may be affected by computer/driver updates. Photon and carbon dose calculation is run on the GPU and must be revalidated after any hardware or software platform changes, including operating system Service Packs. This can be done by running the *RSL-D-RS-9A-SEAT, RayStation 9A System Environment Acceptance Test Protocol*. For photon dose computation, additional validation should be performed by recalculating dose curves for all commissioned treatment machines in the database. (508789)

1.5 VERIFY GPUS FOR COMPUTATIONS ON TREATMENT MACHINES

It is also possible to re-compute photon dose curves for all commissioned machines in the database with the latest major dose engine version and verify that the re-computed dose curves are equal to the dose curves stored in the machine. The re-computation is started by clicking the **Test dose curve computation** button. If the re-computed curves are equal to the saved dose curves, the test will yield a pass. Otherwise, the machines for which the validation failed are listed and the differences can be inspected by the user by creating a copy of the machine in Beam Commissioning and compute new curves manually.

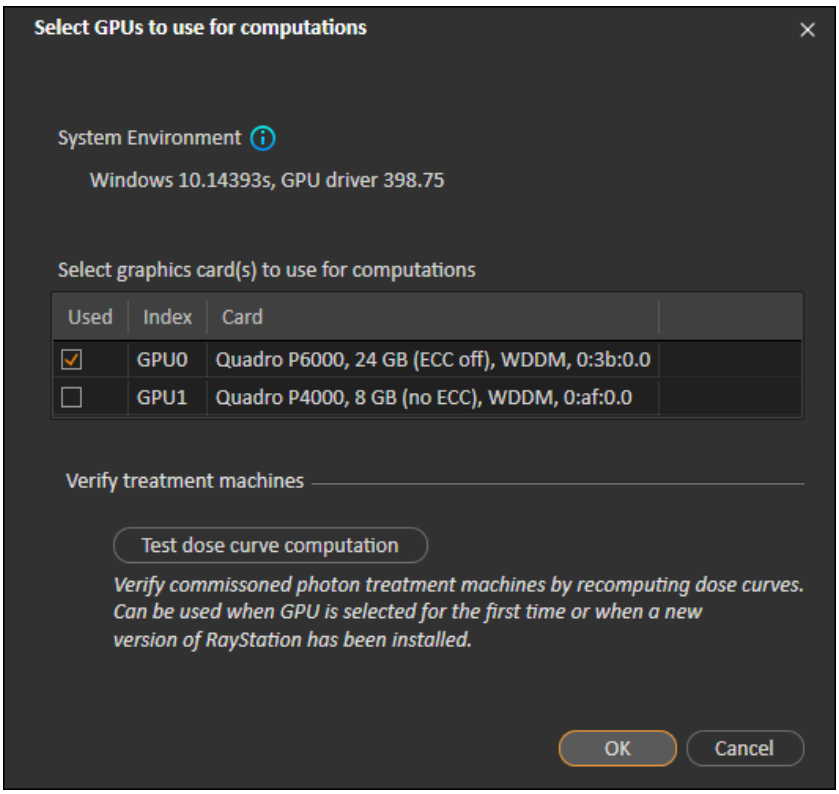

Select GPUs to use for computations
System Environment
Windows 10.14393s, GPU driver 398.75
Select graphics card(s) to use for computations
Used
Index
Card
GPU0
Quadro P6000, 24 GB (ECC off), WDDM, 0:3b:0.0
GPU1
Quadro P4000, 8 GB (no ECC), WDDM, 0:af:0.0
Verify treatment machines
Test dose curve computation
Verify commissoned photon treatment machines by recomputing dose curves. Can be used when GPU is selected for the first time or when a new version of RayStation has been installed.
OK
Cancel

Figure 3. The Select GPUs to use for computations where the Test dose curve computation button is visible.

When comparing the stored dose curve to the re-computed dose curve, a relative difference of 5×10^{-3} is used as pass/fail criterion. For each data point in a dose curve, the relative difference is evaluated according to

$$Abs\left(\frac{d_{recomp} - d_{stored}}{d_{max}}\right) < 5 \cdot 10^{-3}, \qquad \text{[Eq. 1]}$$

where d_{recomp} is the re-computed dose value, d_{stored} is the stored dose value and d_{max} is the maximum dose value in the stored dose curve.

If any data point in the dose curve fails the relative difference criterion, the treatment machine fails the test.

Note: *Between RayStation 4.7 and RayStation 5 centering of wedged dose curves were removed. (See Centering of dose curves on page 95 for more information about dose curve centering). This means that wedged dose curves are computed in slightly different coordinates in RayStation 9A compared to RayStation 4.7 and previous versions. Therefore, wedged dose curves are not used in the test dose curves computation in RayStation 9A. Wedged dose curves can be compared manually by making a copy of the machine, computing dose curves and comparing these to the previous curves. Note that there may be small deviations between previous curves and new curves for wedged curves due to the difference in dose curve centering.*

1.6 LICENCES AND USER GROUPS

RayPhysics can only be opened if the user has a license for RayStation and is added to the Active Directory group "RayStation-BeamCommissioning". (See *RSL-D-RS-9A-USM, RayStation 9A User Manual* for more information).

1.7 DOSIMETRIC INPUT DATA FOR PHOTONS

The beam commissioning procedure needs a set of measurements from the LINAC to be commissioned, as input to the beam model. The set of data is described in the Beam commissioning data spread-sheet and below.

This section does not apply to TomoTherapy LINAC machines.

WARNING!

Beam model quality depends on beam data. The quality of the beam model depends critically on the quality and scope of the beam data, for example, dose curves, output and wedge factors, absolute calibration, phantom size and collimation settings which influence the curve field setup. The entered measurement conditions must match the measurement technique. The sizes of the measured fields should cover the field sizes of the future applications of the beam model.

All input data, such as measured curves and output factors, must be coherent and correspond to the delivery system which is to be commissioned. Otherwise the generated beam model will not be able to calculate a correct dose.

For more information, refer to the *RSL-D-RS-9A-BCDS, RayStation 9A Beam Commissioning Data Specification*. (508979)

The minimum requirement on the input to photon beam commissioning is a set of data all measured with the same source surface distance (SSD), for each photon energy:

- a set of depth dose curves measured in a water phantom for different rectangular field sizes
- cross-plane and/or in-plane dose profiles for different depths and the same field sizes as the depth dose curves
- output factors measured for the same set of field sizes
- an absolute monitor unit calibration
- it is also recommended to have a diagonal profile for the largest field size

1.7.1 Reference point, reference field size and absolute calibration

The absolute dose calibration (dose per monitor units) must be measured at a defined reference point for the reference field size. The SSD for the absolute dose calibration must be the same as used for the dose curves. It is recommended to use a reference point depth which is situated below the region where the electron contamination is important, i.e. at 10 cm.

The reference field size can be set to any value between 9.0 cm to 11.0 cm in both x and y directions and be interpreted symmetrically around the x- and y-axes. For most LINACs the reference field size is 10 cm x 10 cm. Elekta LINACs with the Elekta Beam Modulator cannot create a 10 cm x 10 cm field which is symmetric around the isocenter axis. The standard reference field size for the Elekta Beam Modulator is 9.6 cm x 9.6 cm, 9.6 cm x 10.4 cm, 10.4 cm x 9.6 cm or 10.4 cm x 10.4 cm.

1.7.2 Output factors

Measured output factors must be provided for all field sizes of the measured curves using the same SSD as the absolute calibration point and the curves. As with the absolute calibration, it is recommended to use a reference point which is situated below the region where the electron contamination is important, i.e. at 10 cm. The depth is not required to be the same as for the absolute calibration point. The output factors must all be normalized such that the reference field size (*section 1.7.1 Reference point, reference field size and absolute calibration on page 23*) has output factor 1.

Wedge output factors

The wedge output factor is the dose for the wedged field divided by the dose for the same size open field at the same depth with the same SSD. Wedge output factors must be provided for all wedged curves. They must be measured with the same SSD and at the same depth as the open field output factors. If there are additional, or other, field sizes for the wedged curves, the corresponding open field output factor must also be provided but the open field curves are not required.

Cone output factors

The cone output factors are relative to the open reference field size. Cone output factors must be entered for all cone sizes specified for the machine, and must be measured with the same SSD and at the same depth as the open output factors.

1.7.3 Curves

The curves are water phantom measurements in x (cross-plane), y (in-plane) and z (depth) directions measured during irradiation with rectangular field collimation. The fields must all be reflection symmetric in the inline and the crossline direction, i.e. centralized around the isocenter axis. The field size in x is not required to be the same as the field size in y. It is recommended that the scan resolution be such that the high dose gradient regions are correctly characterized.

The curves can be collimated by jaws only, by MLC only or by MLC and jaws both. The same choice must be made for all curves.

For x-profiles measured with MLC only, be aware that scans below the interleaf-leakage regions will show higher dose values than curves obtained under the leaf. This effect is detector size dependent. The dose curve calculation in RayPhysics 9A does not take the interleaf-leakage into account, therefore it is recommended to perform the scans away from the interleaf-leakage region by a small shift that must be the same for all x-profiles. The shift is saved in the curve file, read by RayStation at dose curve import and automatically mimicked by RayPhysics 9A when computing curves, as described in *Collimation settings for photon curves on page 103* and *section 4.1.7 Rectangular field interpretation on page 106*. The maximum allowed shift is the width of a central MLC leaf or at most 1 cm.

Similarly, scans in the y direction below abutted leaf-ends also show higher dose values in a detector size dependent way. It is recommended to close the leaves away from the central axis (see *Collimation settings for photon curves on page 103* and *section 4.1.7 Rectangular field interpretation on page 106*), even though leaf-tip transmission is part of the dose computation.

Coordinate system

The coordinate system is the IEC 61217 Fixed Reference System defined in *section 2.3.8 Dose curve coordinate system in RayPhysics on page 43*.

Note: *The depth axis runs along the negative z-axis.*

Note: *The gantry and collimator angle of the measured curves are assumed to be zero.*

Supported formats

Supported file formats for the import of dose curves are *.asc/rfa, *.mcc,*.csv, *.snctxt and the Brainlab Monte Carlo data format *.xmcdat.

All formats except *.xmcdat can be opened and reviewed in a text editor. These text formats are described in *Appendix B Dose curve format*. The .xmcdat files cannot be opened in a text editor for review, but are expected to be correctly exported and hence correctly imported into RayPhysics. It is not possible to import diagonal profiles in the *.xmcdat format.

Depth dose curves

The depth dose curves (PDD) must be measured at the central axis and range across all relevant depths (typically 0 cm to 30 cm). One of the curves must be measured with the reference field size (*section 1.7.1 Reference point, reference field size and absolute calibration on page 23*).

Recommended set of field sizes:

2 cm x 2 cm, 3 cm × 3 cm, 5 cm × 5 cm, 10 cm × 10 cm (defined as reference field size), 15 cm × 15 cm, 20 cm × 20 cm, 30 cm × 30 cm, 40 cm × 40 cm, 5 cm × 20 cm and 20 cm × 5 cm.

For an Elekta Beam Modulator the MLC-leaves cannot create these field sizes and the recommended list would instead include:

1.6 cm x 1.6 cm, 2.4 cm × 2.4 cm, 3.2 cm × 3.2 cm, 4 cm × 4 cm, 4.8 cm x 4.8 cm, 7.2 cm × 7.2 cm, 10.4 cm × 10.4 cm (or the selected reference field size), 16 cm × 16 cm, 21 cm × 16 cm, 4.8 cm × 16 cm and 16 cm × 4.8 cm.

Imported data in *.xmcdat format is expected to be measured according to the Brainlab Monte Carlo specification. This is also acceptable when creating a beam model.

The sizes of the measured fields should cover the field sizes of the future application of the beam model.

Enter measurement information

The user should enter information about how the curves were measured. See *section 4.1.5 Measurement conditions on page 101* for more information. It is possible to vary the detector size with field size (one detector width and height per field size, depth dose curves/profiles and open/wedged curves) and taking the detector size into account when computing curves in beam commissioning.

Inline and/or crossline profiles

RayStation commissioning also requires inline and/or crossline profiles for the same field sizes as the depth dose curves and at different depths. The depth of the reference points should preferably be included. Recommended depths are:

d_{max} or $d_{ref.\ point}$, 5 cm, 10 cm and 20 cm

Note: *The field setup for different LINAC models is described in section 4.1.7 Rectangular field interpretation on page 106. Ensure that the field setup at curve measurement corresponds to the field setup in beam commissioning.*

Diagonal profiles

It is also recommended to import at least one diagonal profile for the largest supported field size to correctly model the field corners. There must be a depth dose curve for the same field size imported. Diagonal profiles at several depths can be imported. If only one diagonal profile is imported, it is recommended to use a depth well below the build-up region. The diagonal profiles may have an arbitrary angle (see Figure 4), but this is not supported for all dose curve formats, see *Appendix B Dose curve format* for more information. It is however only possible to import one diagonal angle per field size. It is not possible to import diagonal profiles in *.xmcdat format.

Only diagonal profiles that cross the central axis are supported.

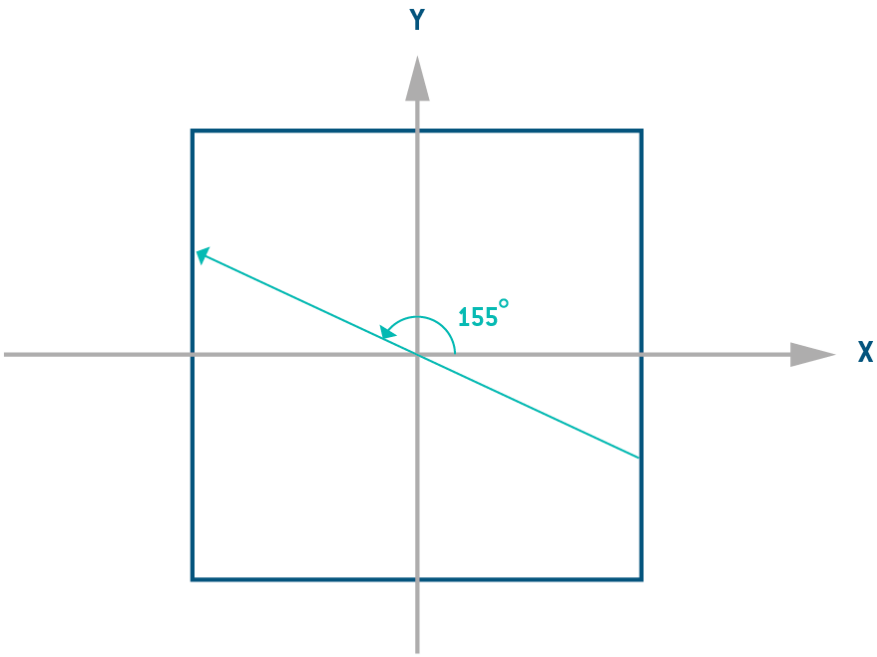


Figure 4. Diagonal angle

Wedged curves

The same requirements apply for wedged curves as for open field curves. In addition, all wedged curves must all be oriented in the same direction (0 degrees, 90 degrees, 180 degrees or 270 degrees), which must also be an allowed direction for the machine.

Cone curves

The following curves are needed for cones:

- Depth dose curves for all cone field sizes (cone diameters) specified for the selected beam quality.
- Inline and/or crossline profiles for all cone field sizes measured at a couple of different depths.

All cone curves must be measured with the same SSD as the open curves. Diagonal profiles are not supported for cones.

1.8 DOSIMETRIC INPUT DATA FOR ELECTRONS

There are three types of measurements necessary for the commissioning of an electron beam quality, i.e., the full model of all applicators to be used for a certain nominal energy.

The first is an open water depth dose curve. This curve is measured without any applicator mounted on the machine, which must typically be done in service mode. The collimators (jaw(s) and MLC) should be retracted. This curve is used to fit the direct electron spectrum of the model.

The second type of measurement is air profiles taken at two different distances from the source with the collimators set to define four different field sizes. These profiles are used to determine the parameters of the electron phase space.

The third type of measurement are depth dose curves and profile curves in water for all applicators. These curves are used to verify and fine-tune the model.

For details about the required measurements, refer to document *RSL-D-RS-9A-BCDS, RayStation 9A Beam Commissioning Data Specification*.

2 DISPLAY OF COORDINATES, MOVEMENTS AND SCALES

RayStation 9A uses the IEC 61217 [1] standard for display of coordinates, movements and scales during treatment planning, with a few exceptions that are user defined. The gantry, collimator and couch angles as well as the field coordinate system may be configured, per LINAC, to be non-IEC see *section 2.3 The treatment machine coordinate system on page 32*.

Note: *Patient positions Head First Supine (HFS), Head First Prone (HFP), Feet First Supine (FFS), Feet First Prone (FFP), Head First Decubitus Left (HFDL), Head First Decubitus Right (HFDR), Feet First Decubitus Left (FFDL) and Feet First Decubitus Right (FFDR) are supported by RayStation 9A.*

In this chapter

This chapter contains the following sections:

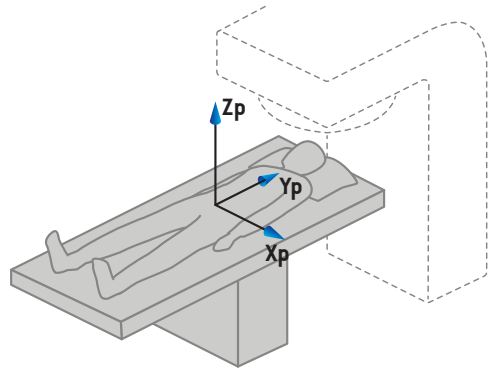
2.1	The patient coordinate system	p. 30
2.2	Patient coordinate system in the DICOM export	p. 31
2.3	The treatment machine coordinate system	p. 32
2.4	The jaw and MLC labeling standard	p. 44

1 IEC 61217:2011 Radiotherapy equipment – Coordinates, movements and scales.

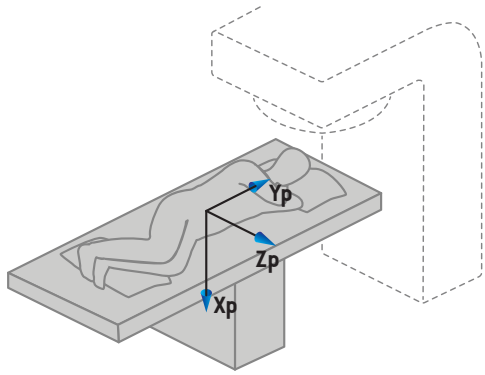
2.1 THE PATIENT COORDINATE SYSTEM

The patient coordinate system is oriented with the positive x-axis towards the patient's left arm, the positive y-axis towards the patient head and the positive z-axis in the anterior direction. The coordinate system follows the patient orientation: head first or feet first, supine or prone, decubitus right or decubitus left. In the hierarchy of IEC 61217 coordinate systems, the patient coordinate system has the table top coordinate system as its mother system.

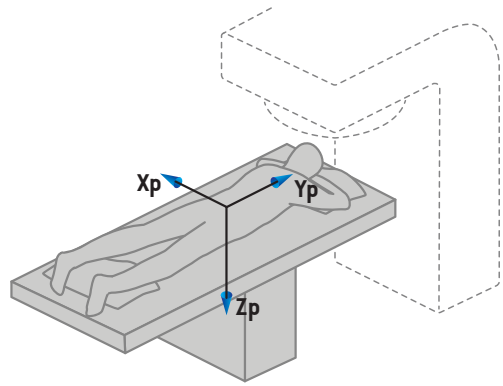
The RayStation 9A dose and the dose difference distributions are all visualized in the patient coordinate system. In general, in RayStation 9A the patient coordinates are reported as **Right-Left**, **R-L** (right-left = x -/+), **Inf-Sup**, **I-S** (inferior-superior = y -/+) and **Post-Ant**, **P-A** (posterior-anterior = z -/+).



A) Head First Supine



B) Head First Decubitus Left

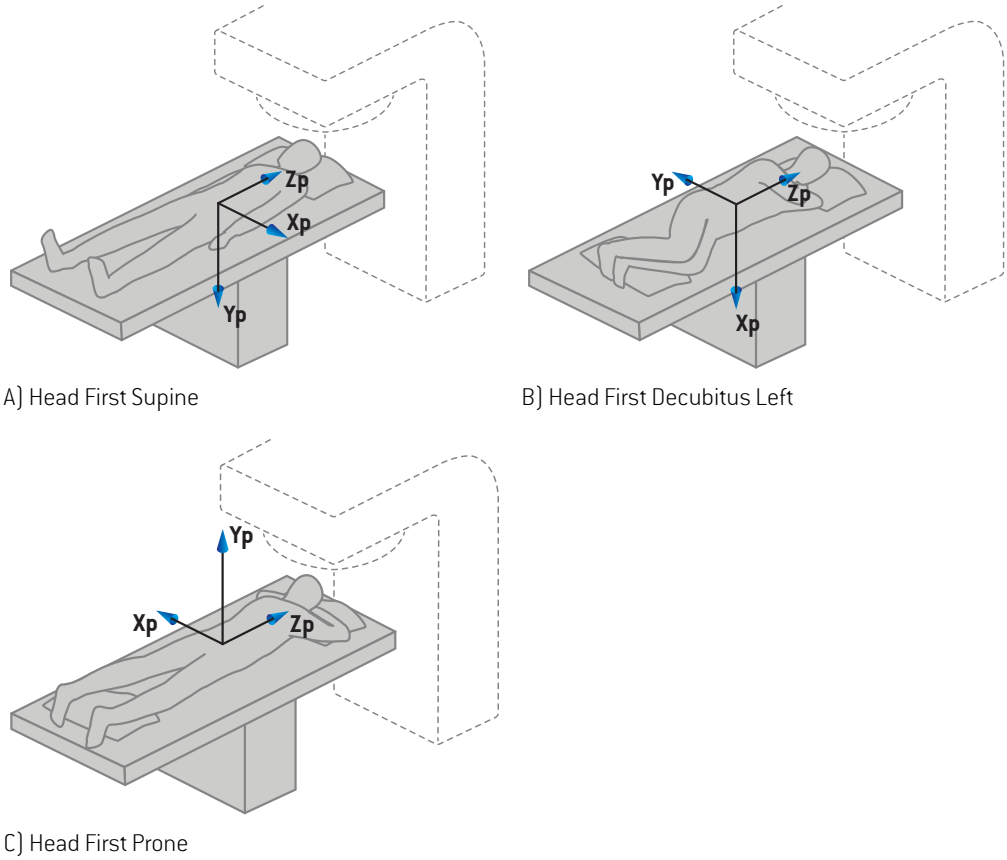


C) Head First Prone

Figure 5. The patient coordinate system. Some examples of supported positions are illustrated: A) Head First Supine (HFS), B) Head First Decubitus Left (HFDL) and C) Head First Prone (HFP).

2.2 PATIENT COORDINATE SYSTEM IN THE DICOM EXPORT

Patient coordinates in DICOM exported data sets follow the DICOM standard, with the positive x-axis towards the patients left arm, the positive z-axis towards the patient head and the positive y-axis in the posterior direction. The coordinate system follows the patient orientation: head first or feet first, supine or prone, decubitus right or decubitus left.



A) Head First Supine

B) Head First Decubitus Left

C) Head First Prone

Figure 6. The patient coordinate system in the DICOM export follows the DICOM standard. Some examples of supported positions are illustrated: A) Head First Supine (HFS), B) Head First Decubitus Left (HFDL) and C) Head First Prone (HFP).

2.3 THE TREATMENT MACHINE COORDINATE SYSTEM

RayStation 9A uses the IEC 61217 standard for display of LINAC coordinates, movements and scales during treatment planning, with the exception of gantry, collimator and couch angles as well as the field coordinate systems, which may be configured, per LINAC, to be non-IEC. There are also two options for jaw labeling.

2.3.1 The machine coordinate systems overview

The machine coordinate systems in IEC 61217 are a set of coordinate systems, each defined in relation to its mother coordinate system, starting with a fixed coordinate system which has the origin at the isocenter, the positive x direction to the right for an observer facing the gantry, the positive y-axis from the isocenter towards the gantry along the axis of gantry rotation and the positive z-axis directed upwards from the isocenter.

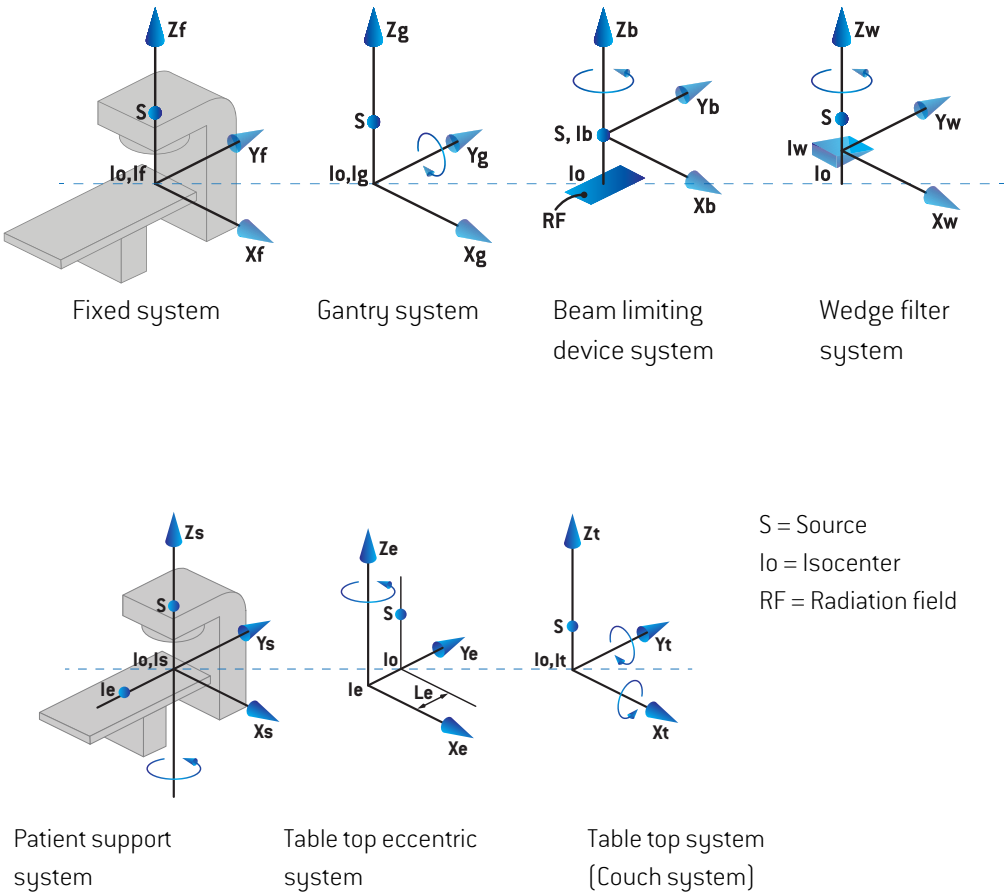


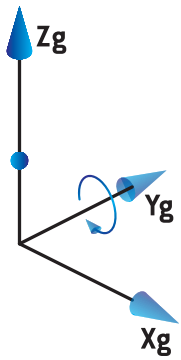
Figure 7. The machine coordinate systems according to the IEC 61217 standard.

If the machine is commissioned to replace the couch rotation by the ring rotation (e.g., the Vero machine), the rotation around the Zs axis in the patient support coordinate system is replaced by a rotation in the opposite direction around the Zg axis in the gantry coordinate system. The relationship between the patient and the gantry systems is thus maintained.

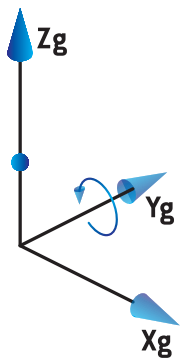
2.3.2 The gantry coordinate system

The gantry coordinate system rotates with the gantry. The gantry coordinate system has the fixed coordinate system as its mother system.

- For **IEC standard**, it is defined to coincide with the fixed coordinate system when the gantry angle is zero. The gantry angle increases gradually for clockwise rotation as viewed by an observer facing the gantry.



- For **Non-IEC gantry scale (Varian Standard)**, the gantry angle is 180 degrees when the beam enters from above. The gantry angle increases gradually for counter clockwise rotation as viewed by an observer facing the gantry.



Note: *If a LINAC is configured to use gantry angle as IEC 61217, the angle unit is given as [deg].*

Note: *If a LINAC is configured to use gantry angle as Non-IEC ("Varian Standard"), the angle unit is given as [deg Non-IEC].*

2.3.3 The beam limiting device coordinate system

The beam limiting device coordinate system is fixed in the gantry beam limiting device. The beam limiting device coordinate system has the gantry coordinate system as its mother system.

There are three settings in RayPhysics that affect the behavior of angles, positions and names in this coordinate system; the **Gantry and collimator coordinate system definitions**, the **Field coordinate system definitions** and the **Jaw labeling standard**. If all three settings are set to "IEC 61217", the definitions are consistent with those in the IEC 61217 standard.

The Gantry and collimator coordinate system definitions setting

The **Gantry and collimator coordinate system definitions** setting in RayPhysics controls the reporting of the beam limiting device rotation angle:

- For **IEC standard**, the axes coincide with the gantry system when the collimator angle is zero. The collimator angle is defined to be positive for counterclockwise rotation in the Beam's eye view, i.e. when viewed from the source. For this coordinate system, the collimator angle is usually 180 degrees when the tray opening is facing the gantry for Varian machines.
- The **Non-IEC (Varian Standard)** collimator coordinate system is rotated 180 degrees compared to the IEC standard and the collimator angle is defined to be positive for a clockwise rotation in the Beam's eye view, i.e. when viewed from the source. For this coordinate system, the collimator angle is usually zero degrees when the tray opening is facing the gantry for Varian machines.

Note: *If a LINAC is configured to use a collimator angle as IEC 61217, the angle unit is given as [deg].*

Note: *If a LINAC is configured to use a collimator angle as Non-IEC, the angle unit is given as [deg Non-IEC].*

The Field coordinate system definitions setting

The **Field coordinate system definitions** setting in RayPhysics defines how jaw and MLC leaf positions are reported and defined. The following description uses jaw naming convention according to the IEC 61217 standard.

Note: *If a LINAC is configured to use field coordinate system as IEC 61217, the unit for jaw and leaf positions is given as [cm].*

Note: *If a LINAC is configured to use field coordinate system as Non-IEC, the unit for jaw and leaf positions is given as [cm Non-IEC].*

Collimator positions according to IEC 61217

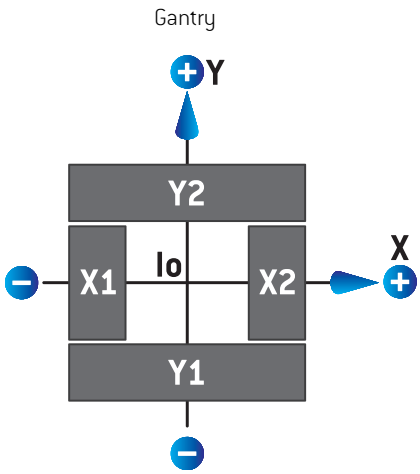


Figure 8. The collimator positions in the Beam's eye view according to the IEC 61217 standard.

The collimator positions according to the IEC 61217 standard, for a beam with (IEC) collimator angle 0 when viewed from the source, are described in the table below.

When the edge of…	is positioned to the…	of the isocenter axis, its position reading value is…
X1, X2 (jaw or MLCX leaf)	right	positive
X1, X2 (jaw or MLCX leaf)	left	negative
Y1, Y2 (jaw or MLCY leaf)	gantry side	positive
Y1, Y2 (jaw or MLCY leaf)	non-gantry side	negative

Collimator positions according to Non-IEC (Varian Standard)

For Non-IEC, positive position coordinates are reported in all directions for jaws and leaves that have not crossed the center line. That is, negative coordinates are reported for overtravel.

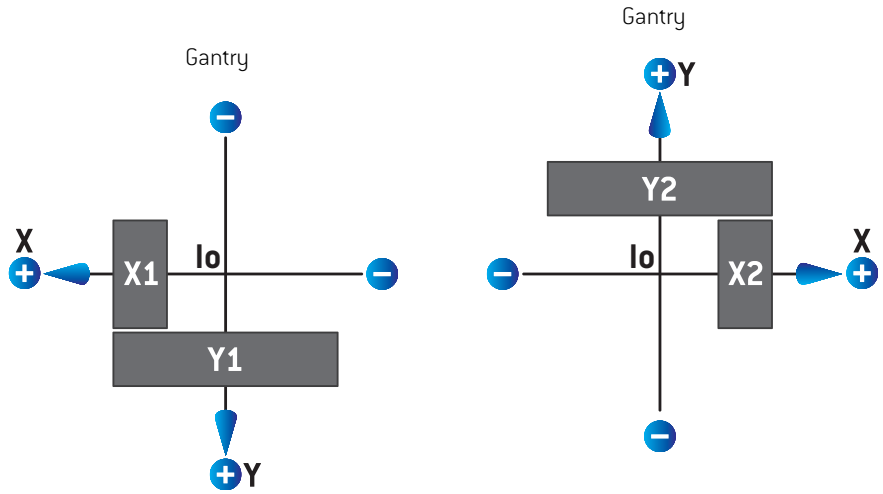


Figure 9. The collimator positions in the Beam's eye view according to the Non-IEC (Varian Standard). Note that the coordinates visualized in the Beam's eye view in RayStation always uses the IEC 61217 coordinate system.

The collimator positions according to Non-IEC (Varian Standard), for a beam with (IEC) collimator angle 0 when viewed from the source, are described in the table below.

When the edge of…	is positioned to the…	of the isocenter axis, its position reading value is…
X1 (jaw or MLCX leaf)	right	negative
X1 (jaw or MLCX leaf)	left	positive
X2 (jaw or MLCX leaf)	right	positive
X2 (jaw or MLCX leaf)	left	negative
Y1 (jaw or MLCY leaf)	gantry side	negative
Y1 (jaw or MLCY leaf)	non-gantry side	positive
Y2 (jaw or MLCY leaf)	gantry side	positive
Y2 (jaw or MLCY leaf)	non-gantry side	negative

The Jaw labeling standard setting

The **Jaw labeling standard** setting in RayPhysics is described in *section 2.4 The jaw and MLC labeling standard on page 44*.

2.3.4 The wedge filter coordinate system

The wedge filter coordinate system rotates with the wedge and the positive y axis points from heel to toe of the wedge. The wedge filter coordinate system has the beam limiting device coordinate system as its mother system. In RayPhysics and the main RayStation 9A application, the wedge coordinate system is defined to coincide with the selected collimator coordinate system (IEC 61217 or Non-IEC) for a wedge orientation of zero degrees.

- For collimator coordinate system **IEC 61217**, the wedge orientation is zero degrees when the toe points towards the gantry for collimator angle zero.
- For collimator coordinate system **Non-IEC**, the wedge orientation is zero degrees Non-IEC when the toe points away from the gantry for collimator angle zero degrees Non-IEC.

The wedge orientation increases gradually for a counter-clockwise rotation.

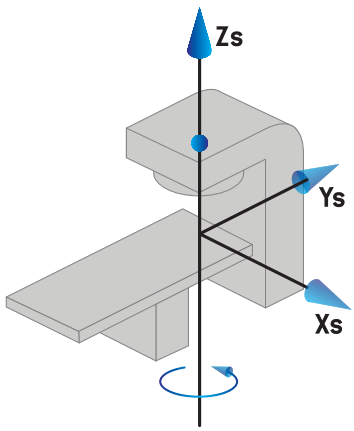
Note: *If a LINAC is configured to use a collimator angle as IEC 61217, the wedge orientation angle unit is given as [deg].*

Note: *If a LINAC is configured to use a collimator angle as Non-IEC, the wedge orientation angle unit is given as [deg Non-IEC].*

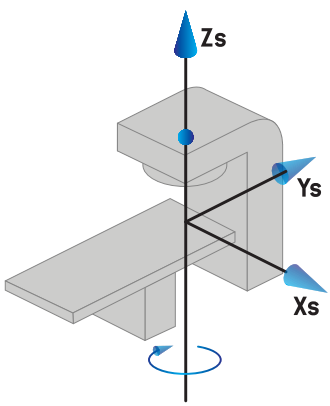
2.3.5 The patient support coordinate system

The patient support coordinate system rotates with the part of the patient support that rotates around the vertical axis Zs. The patient support coordinate system has the fixed coordinate system as its mother system.

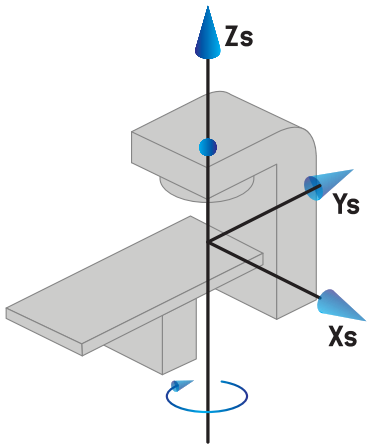
- For **IEC standard**, the patient support system coincides with the fixed system when the couch angle is zero. The positive rotation direction is defined to be counter-clockwise as seen from above.



- For **Non-IEC 1 (Varian IEC)** machine scale, the patient support system coincides with the fixed system when the couch angle is zero. The positive rotation direction is defined to be clockwise as seen from above.



- For **Non-IEC 2 (Varian Standard)** machine scale, the couch angle is 180 degrees when the IEC couch angle is zero degrees. The positive rotation direction is defined to be clockwise as seen from above.



Note: *If a LINAC is configured to use couch angle as IEC 61217, the angle unit is given as [deg].*

Note: *If a LINAC is configured to use couch angle as Non-IEC 1 ("Varian IEC"), the angle unit is given as [deg Non-IEC] in the user interface and as [deg Non-IEC CW] in plan reports.*

Note: *If a LINAC is configured to use couch angle as Non-IEC 2 ("Varian Standard"), the angle unit is given as [deg Non-IEC] in the user interface and as [deg Non-IEC CW] in plan reports.*

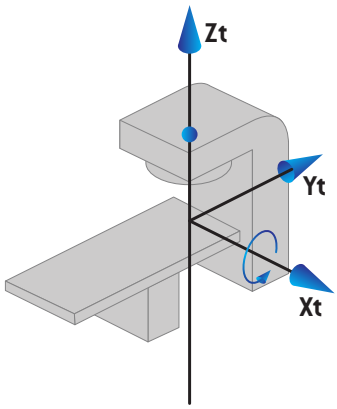
2.3.6 The table top eccentric coordinate system

In RayStation, only zero degrees eccentric table top rotation angle and zero translation distance are supported, and thus the table top eccentric coordinate system always coincides with the patient support coordinate system. The table top eccentric coordinate system has the patient support coordinate system as its mother system.

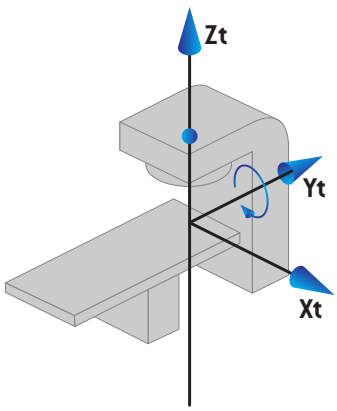
2.3.7 The table top coordinate system

In RayStation, the table top coordinate system has the table top eccentric coordinate system as its mother system. Pitch and roll angles are always expressed using the IEC standard.

- The table top pitch angle is defined as the rotation about axis Xt. An increase in the pitch angle corresponds to the clockwise rotation of the table top as viewed from the table top coordinate system origin along the positive Xt axis.



- The table top roll angle is defined as the rotation about axis Yt. An increase in the roll angle corresponds to the clockwise rotation of the table top as viewed from the table top coordinate system origin along the positive Yt axis.



2.3.8 Dose curve coordinate system in RayPhysics

The Beam Commissioning module has a dose curve coordinate system corresponding to the IEC gantry coordinate system, translated so that the origin is on the isocenter axis at the surface of the water phantom. The x-axis is aligned with the cross-line axis. The y-axis is aligned with the inline axis, with the positive direction towards the gantry. The negative z-direction, from source towards isocenter, is aligned with the depth direction. The gantry and collimator angles are always assumed to be zero degrees for the dose curves in the Beam Commissioning module. The model is fully reflection symmetric in the xz- and the yz-plane, whereas measurements can sometimes be mildly asymmetric.

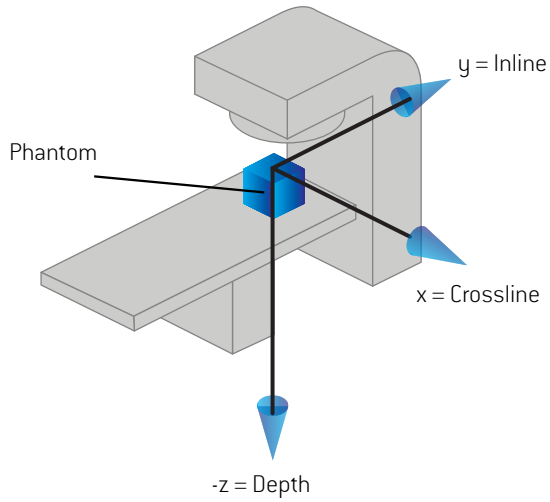


Figure 10. The dose curve coordinate system.

2.4 THE JAW AND MLC LABELING STANDARD

In RayStation 9A the jaws can be labeled according to one of the standards IEC 61217 or IEC 601-2-1. The description in this section uses the IEC 61217 Field coordinate system definitions setting.

2.4.1 The IEC 61217 jaw labeling standard

In **IEC 61217**, Y2 is close to the gantry and Y1 is away from the gantry, X1 is to the left and X2 to the right for an observer facing the gantry with gantry and collimator angle zero in the IEC 61217 coordinate system.

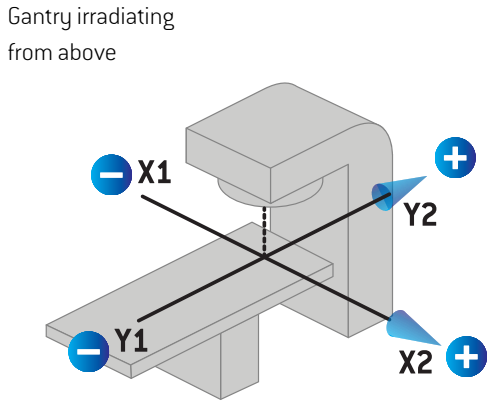


Figure 11. The jaw and MLC labels (IEC 61217).

2.4.2 The IEC 601 jaw labeling standard

In **IEC 601**, X1 is close to the gantry and X2 is away from the gantry, Y2 is to the left and Y1 to the right for an observer facing the gantry with gantry and collimator angle zero in the IEC 61217 coordinate system.

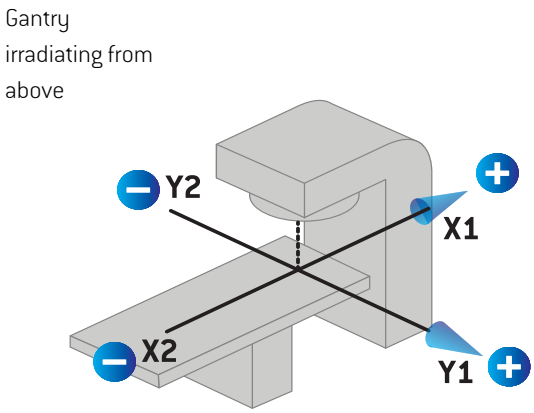


Figure 12. The jaw and MLC labels (IEC 601).

Note: *The jaw labeling standard setting only affects the names of the collimators in RayStation and the Machine properties workspace in RayPhysics. Note that the coordinate axes are still labeled according to IEC 61217, examples being the dose curve labels and parameters in the Beam model workspace in RayPhysics.*

3 THE BEAM COMMISSIONING MODULE

This chapter describes the workspaces in the Beam Commissioning module.

In this chapter

This chapter contains the following sections:

3.1	Beam Commissioning user interface	p. 50
3.2	Machine tree view	p. 54
3.3	Operations on machines	p. 58
3.4	Add new beam quality	p. 60
3.5	Machine constraints workspace	p. 66
3.6	Photon beam model workspaces for C-arm LINACs	p. 67
3.7	Photon beam model workspaces for TomoTherapy LINACs	p. 71
3.8	Electron beam model workspaces for C-arm LINACs	p. 75
3.9	Proton and carbon ion beam model workspaces	p. 85

WARNING!

Beam models must be validated before clinical use. It is the responsibility of the user to validate and commission all beam models before they are used to create clinical treatment plans.

RayStation 9A is developed to be used by trained Radiation Oncology professionals. We strongly suggest that users adhere to recommendations published in AAPM TG40, TG142, TG53, IAEA TRS 430, IAEA TRS 483 and other standards to assure accurate treatment plans.

Computed dose accuracy depends directly on the beam model quality. Beam model insufficiency may lead to deviations between approved and delivered dose. All parameter values and plan QA and QC shall be reviewed and approved by qualified physicists. The dose calculation must be validated for all commissioned CT machines.

- The computed dose shall be validated for all relevant clinical situations including, but not limited to, variation in SAD, SSD, field-size, field-shape, off-axis position (x, y and diagonal), collimation type, degree of modulation, leakage dose (variation in MU/Gy or NP/Gy), couch/gantry/collimator angles, patient/phantom material composition and patient/phantom material geometry.
- Known limitations are described in the *RSL-D-RS-9A-REF, RayStation 9A Reference Manual*. Additional limits of operation for each beam model must be identified during validation and adhered to during planning.

For photons:

Special care should be taken before using RayStation 9A with MLC leaves smaller than 5 mm, materials that differ from common patient materials, blocks, wedges (in particular off-axis wedges), complex VMAT plans, rotational plans with small field sizes, Siemens mARC plans and wave arc plans, especially with larger ring rotation than 15 degrees.

Note that:

- a beam model validated for 3D-CRT is not necessarily suitable for IMRT plans.
- a beam model validated for SMLC is not necessarily suitable for DMLC plans.
- a beam model validated for SMLC or DMLC is not necessarily suitable for VMAT plans.
- a beam model validated for VMAT is not necessarily suitable for plans created using sliding window VMAT sequencing.

Validation must be performed for each selected treatment technique using Beam 3D modeling or RayStation. For C-arm LINACs, see warning 508998 and 530330. For TomoTherapy treatment machines, see also warning 252208.

For protons:

Validation shall include relevant compensator and range shifter geometries, block and/or MLC aperture contours, air gaps/snout positions, isocenter to surface distance, spot tune and patterns, spread out bragg peak depth and modulation width, field sizes (see also warning 371600).

For Mevion Hyperscan, see also warning 369009.

For carbon ions:

Validation shall include relevant range shifters, air gaps/snout positions, isocenter to surface distances, spot tune and patterns, ranges, field sizes (see also warning 371600).

For electrons:

Validation shall include relevant applicator geometries, field sizes without cutout, field shape orientation for rectangular applicators, cutout material and thickness, correct airgap to isocenter, correct D50 water range per nominal beam energy, correct field shape for field with cutout. Only Cerrobend cutouts with straight edges, i.e., parallel to the beam axis line, are supported. (508815)

3.1 BEAM COMMISSIONING USER INTERFACE

The Beam Commissioning module user interface has the machine tree view workspace to the left and the parameter workspaces to the right. The relative size of the two workspaces can be changed by putting the cursor on top of the border between the two workspaces, but not on the arrow.

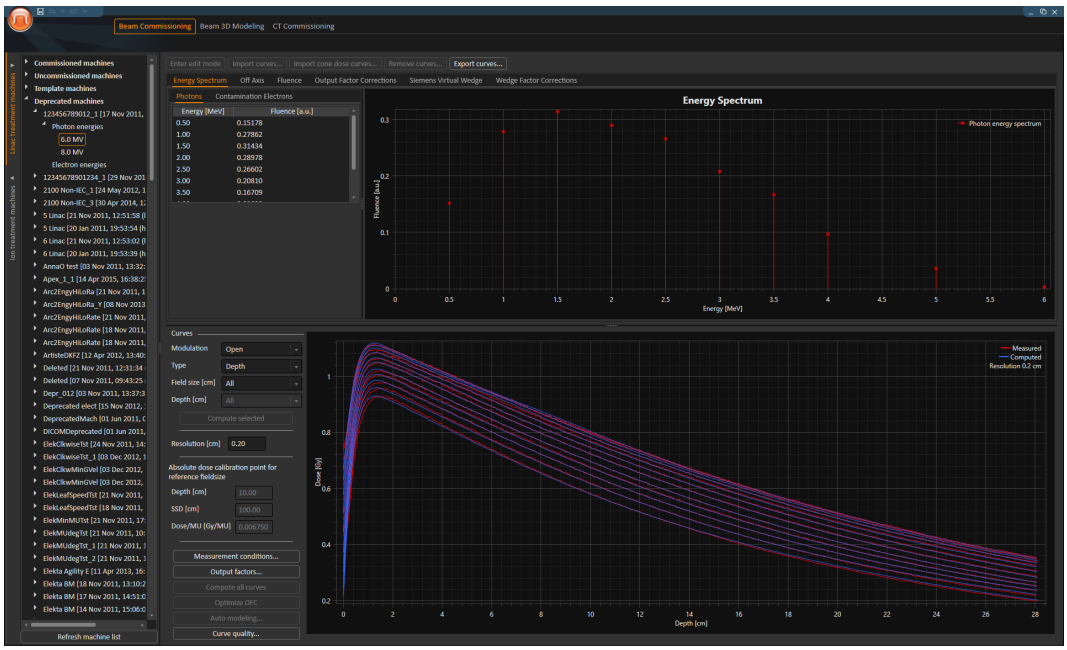


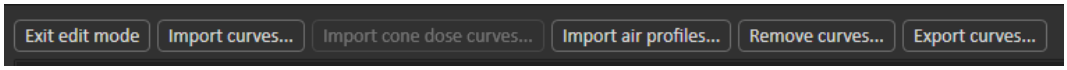
Figure 13. The Beam Commissioning module workspace.

3.1.1 Operations on graphs

The following mouse commands are available in all graphs in the Beam Commissioning and CT Commissioning modules:

- Left-click on a curve or a stem plot marker to open an annotation that displays the name of the data series and the x- and y-values.
- Hold down the middle mouse button, or the mouse scroll wheel, while moving the mouse to define an area to zoom in to. It is also possible to zoom in and out the entire graph using the scroll wheel.
- Click on the right mouse button to open the plot's context menu.
- Use the **AutoZoom** command to reset the plot. The plot can also be reset by pressing A or double-clicking the middle mouse button.
- Type Ctrl + C to copy the plot to the clipboard.
- Type Ctrl + Alt + R to write a plot report to the clipboard. The plot report includes the curve data for all curves in the plot with x- and y-values separated by vertical lines.
- Use Ctrl + V to paste the plot or the plot report from the clipboard to a document or text file.
- Right-click in a dose curve graph and select **Swap background color** to change between black and white background color of the dose curve graphs. Default is black background color. If the background color is swapped, the selection will apply to all dose curve graphs in the current RayPhysics session.

3.1.2 The top bar for LINAC machines



- **Enter edit mode** - opens the machine for editing and locks it to prevent other users from editing the same machine.
- **Exit edit mode** - closes the machine edit mode and opens it for editing of other users.
- **Import curves** - opens a dialog which allows the user to browse for measured dose curves to be imported. For more information, see *section 4.1.2 Import curves on page 90*. Not applicable for TomoTherapy LINAC machines.
- **Remove curves** - opens a dialog which allows the user to delete imported curves.
- **Export curves** - opens a dialog where the user can select a directory to which the files are to be exported. For more information, see *section 4.1.3 Export curves on page 97*.
- **Import cone dose curves** - opens a dialog which allows the user to browse for measured cone dose curves to be imported. Only enabled for photon beam qualities with added cones. Not applicable for TomoTherapy LINAC machines.
- **Import air profiles** - opens a dialog which allows the user to browse for measured air profiles to be imported. Only enabled for electron beam qualities. Not applicable for TomoTherapy LINAC machines.

3.1.3 The top bar for Ion treatment machines

- **Enter edit mode** - opens the machine for editing and locks it to prevent other users from editing the same machine.
- **Exit edit mode** - closes the machine edit mode and opens it for editing of other users.
- **Import curves** - opens a dialog which allows the user to browse for measured dose curves to be imported. For more information, see *Import curves on page 288*. Only applicable for PBS machines and Line scanning.
- **Remove curves** - opens a dialog which allows the user to delete imported curves. Only applicable for PBS machines and Line scanning.
- **Export curves** - opens a dialog where the user can select a directory to which the files are to be exported. For more information, see *Export curves on page 288*. Only applicable for PBS machines and Line scanning.
- **Automodel** - allows the user to create a machine model based on the imported beam data. For more information, see *section 6.2.5 Auto-modeling of proton beam model parameters on page 291*. Only applicable for PBS machines and Line scanning.

3.2 MACHINE TREE VIEW

The machine tree view shows the available treatment machines. There are three groups of treatment machines: LINAC treatment machines, Ion treatment machines and NCT treatment machines. Select to view machine geometry and planning constraints for a machine by clicking the machine name in the list.

For LINAC treatment machines: Select to view the beam model parameters for a specific machine by expanding the tree view and clicking the beam quality of the machine, for instance 6 MV.

For Ion treatment machines: Select to view the beam model parameters for a specific machine by expanding the tree view and clicking the beam quality of the machine, indicated by the treatment technique. For Uniform Scanning, Double Scattering and Wobbling machines only a subset of the beam model parameters are visible.

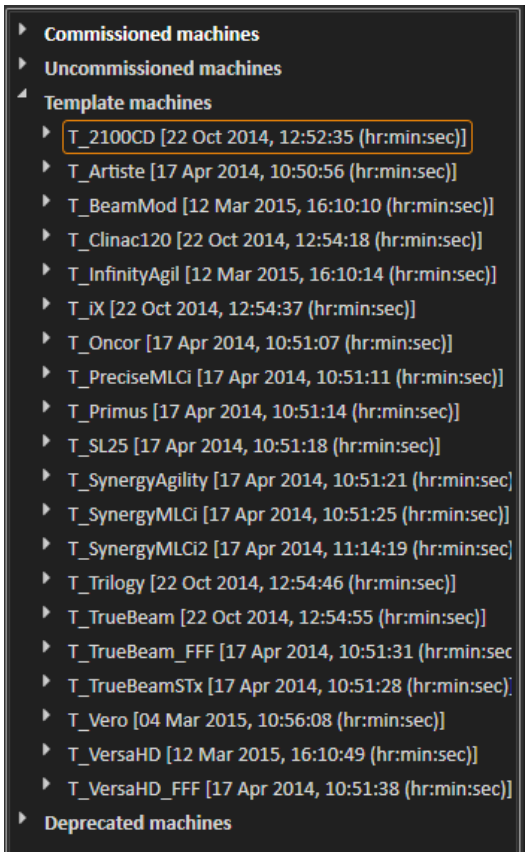

Commissioned machines
Uncommissioned machines
Template machines
T_2100CD [22 Oct 2014, 12:52:35 (hr:min:sec)]
T_Artiste [17 Apr 2014, 10:50:56 (hr:min:sec)]
T_BeamMod [12 Mar 2015, 16:10:10 (hr:min:sec)]
T_Clinac120 [22 Oct 2014, 12:54:18 (hr:min:sec)]
T_InfinityAgil [12 Mar 2015, 16:10:14 (hr:min:sec)]
T_iX [22 Oct 2014, 12:54:37 (hr:min:sec)]
T_Oncor [17 Apr 2014, 10:51:07 (hr:min:sec)]
T_PreciseMLCi [17 Apr 2014, 10:51:11 (hr:min:sec)]
T_Primus [17 Apr 2014, 10:51:14 (hr:min:sec)]
T_SL25 [17 Apr 2014, 10:51:18 (hr:min:sec)]
T_SynergyAgility [17 Apr 2014, 10:51:21 (hr:min:sec
T_SynergyMLCi [17 Apr 2014, 10:51:25 (hr:min:sec)]
T_SynergyMLCi2 [17 Apr 2014, 11:14:19 (hr:min:sec
T_Trilogy [22 Oct 2014, 12:54:46 (hr:min:sec)]
T_TrueBeam [22 Oct 2014, 12:54:55 (hr:min:sec)]
T_TrueBeam_FFF [17 Apr 2014, 10:51:31 (hr:min:sec
T_TrueBeamSTx [17 Apr 2014, 10:51:28 (hr:min:sec)
T_Vero [04 Mar 2015, 10:56:08 (hr:min:sec)]
T_VersaHD [12 Mar 2015, 16:10:49 (hr:min:sec)]
T_VersaHD_FFF [17 Apr 2014, 10:51:38 (hr:min:sec)]
Deprecated machines

Figure 14. The machine tree view.

When opening the Beam Commissioning module the machine tree view shows the available machines in the machine database. From this state the machines are changed locally by the user.

Note: *When leaving edit mode, the undo-redo history will be cleared.*

3.2.1 Machine status

In the machine tree in the Beam Commissioning module, there is a list of the machines available in the machine database. There are four types of machines:

- **Template machines** - model machines for different machine types. The template machines are included in the database at installation and can be used as a starting point when creating a machine model at the clinic. Template machines do not have measured dose curves. Template machines cannot be edited until copied. The template machines cannot be used within RayStation.

  Note: *Always verify that your machine model is correctly characterized. Template machines should never be used without careful verification of physical parameters.*

- **Commissioned machines** - machines at the clinic for which the beam commissioning procedure is finished. These machines are ready for treatment planning in RayStation. Commissioned machines cannot be edited.
- **Uncommissioned machines** - machines at the user clinic where the beam commissioning has not yet been completed. Uncommissioned machines can be edited and cannot be used for plan generation in RayStation.
- **Deprecated machines** - previously commissioned machines that are no longer eligible for plan generation. It is not possible to re-compute doses calculated with a deprecated machine. Deprecated machines cannot be edited.

3.2.2 Save to and read from database

Machines are saved to the machine database at save, commissioning, deprecate or delete and optionally at **Exit edit mode**. Saving machines requires synchronization with the machine database, which may have been changed by another user. The synchronization can also be forced by clicking the **Refresh machine list** at the bottom of the machine list workspace.

Opening a machine in edit mode also triggers an automatic synchronization with the database.

3.3 OPERATIONS ON MACHINES

Right-clicking on a machine name will give access to a few options.

Commissioned, uncommissioned, template or deprecated machine

For a commissioned, uncommissioned, template or deprecated machine:

- **Create machine report** - creates a report containing all the machine parameters and curves. Not applicable for Ion treatment machines or TomoTherapy LINAC machines.
- **Create machine report (without dose curves)** - creates a report containing all the machine parameters. Not applicable for Ion treatment machines or TomoTherapy LINAC machines.
- **Copy** - copies the machine to the uncommissioned machines, allowing the user to edit the machine properties. Note that identical machine names are not allowed (for non-deprecated machines); when copying a machine, the name is copied and suffixes with version numbers are added to the end of the name. Long machine names are also truncated to at most 16 characters.
- **Copy beam quality** - copies the selected beam quality. Use **Paste beam quality** on an uncommissioned machine to add the beam quality to the machine. Not applicable for Ion treatment machines or TomoTherapy LINAC machines.

Note: *Only photon beam quality parameters will be written in the report. For electron beam qualities, only the dose curves will be written.*

Uncommissioned machine

For an uncommissioned machine:

- **Commission** - opens a dialog that will guide the user through all machine parameters before a password protected commissioning step. This moves the uncommissioned machine to the commissioned machines, making it impossible to edit the machine and making the machine eligible for clinical planning and dose computation. Not applicable for Ion treatment machines.
- **Delete** - deletes the machine from the machine database. Once the machine has been deleted the operation cannot be reversed.
- **Move to group** – opens a dialog where the uncommisioned machine can be moved to a machine group. Select an existing group from the drop-down list or create a new group by entering a name in the text field. To remove a machine from a group, select group 'None'. Not applicable for Ion treatment machines or TomoTherapy LINAC machines.
- **Paste beam quality** - pastes a copied beam quality to the machine. All dose curves will be removed for the new beam quality. Not applicable for Ion treatment machines or TomoTherapy LINAC machines.
- **Add new beam quality** - open a dialog to create a new beam quality for the machine. Right-click on **Photon energies** to add a new photon beam quality, and right-click on **Electron energies** to add a new electron beam quality. For more information, see section *section 3.4 Add new*

beam quality on page 60. Not applicable for Ion treatment machines or TomoTherapy LINAC machines.

Commissioned machine

Additional alternative for a commissioned machine:

- **Deprecate** - moves the machine to the deprecated machines. This removes the machine from the clinical mode, but will allow older plans to be loaded so that doses can be reviewed.

Uncommissioned machine

Right-clicking on a beam quality for an uncommissioned machine with several beam qualities gives access to:

- **Delete beam quality** - deletes the beam quality from the machine. Not applicable for Ion treatment machines or TomoTherapy LINAC machines.

Right-clicking on an applicator for an uncommissioned machine with an electron beam quality gives access to:

- **Delete applicator** - deletes the applicator from the electron beam quality. Not applicable for Ion treatment machines or TomoTherapy LINAC machines.

3.4 ADD NEW BEAM QUALITY

This section describes how to add a new beam quality for LINAC treatment machines. This procedure is not applicable for Ion treatment machines or TomoTherapy LINAC machines.

In this section

This section contains the following sub-sections:

3.4.1	Add photon beam quality	p. 61
3.4.2	Add electron beam quality	p. 65

3.4.1 Add photon beam quality

Introduction

When adding a new photon beam quality, both the nominal energy and the internally used dose computation energy have to be specified. For most users the nominal energy should be set to the same value as the dose computation energy. However, in some cases it is also possible to set a different nominal energy than the dose computation energy. In those cases it is important to read and understand the warning below.

When adding a new photon beam quality, it is also possible to select a non-standard fluence mode for the beam quality.

Nominal energy

In RayPhysics the nominal energy is used in the machine tree view, for all energy specific properties in the machine constraints workspace, for dose curve import and dose curve export. In RayStation the nominal energy is displayed in the user interface, is used for energy selection, used in reports and as DICOM Nominal Beam Energy in both DICOM import and export.

Nominal energies between 4 MV and 25 MV are supported. It is not possible to change the nominal energy after the beam quality has been added.

Dose computation energy

The dose computation energy will be used to get the maximum allowed energy bins in the photon energy spectrum (see *Photon energy spectrum on page 146*) and hence sets the maximum allowed point spread kernel for photon dose computation. The dose computation energy is also used to select the correct GSTT parameters for dose computation with Varian Enhanced Dynamic wedge.

Dose computation energies between 4 MV and 20 MV are supported. It is not possible to change the dose computation energy after the beam quality has been added.

Fluence mode

It is possible to select that a beam quality shall have one of the two non-standard fluence modes FFF (flattening filter free) or SRS (stereotactic radiosurgery).

Setting a non standard fluence mode (FFF/SRS) will ensure that when a plan using this beam quality is DICOM exported, information about the non-standard fluence mode is included in the RTPlan.

Note that setting a non-standard fluence mode will not in any other way affect the beam model or dose calculation.

For more information about how to model a flattening filter free beam, see *section 4.8.5 Flattening filter free beam model on page 196*.

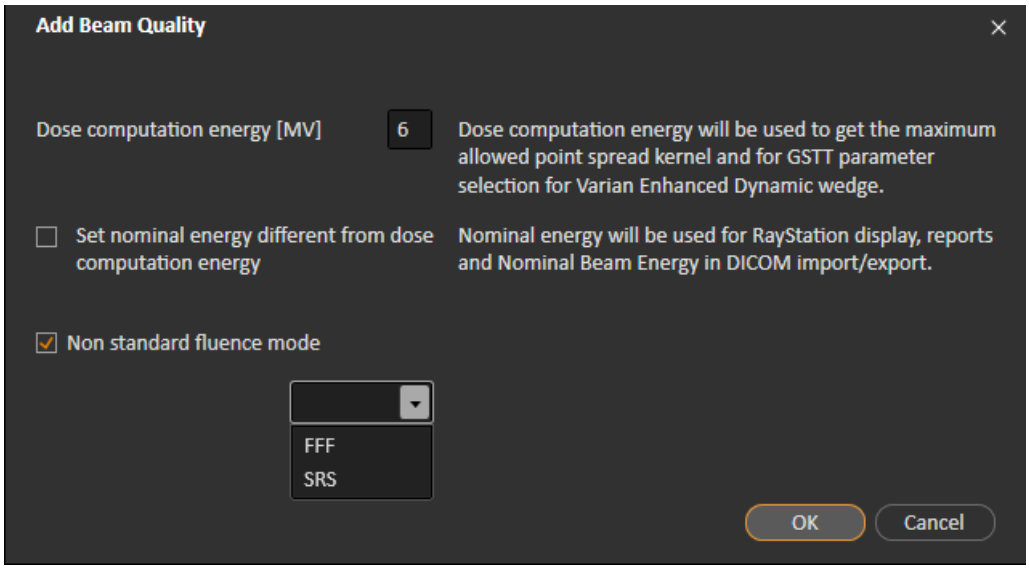

Add Beam Quality
Dose computation energy [MV]
6
Dose computation energy will be used to get the maximum allowed point spread kernel and for GSTT parameter selection for Varian Enhanced Dynamic wedge.
Set nominal energy different from dose computation energy
Nominal energy will be used for RayStation display, reports and Nominal Beam Energy in DICOM import/export.
Non standard fluence mode
FFF
SRS
OK
Cancel

Figure 15. Adding a photon beam quality with non standard fluence mode.

Precautions

WARNING!

Dose computation photon beam energy and nominal photon beam energy. The RayStation photon dose computation internally uses a photon energy definition according to BJR #11 (British Journal of Radiology supplement number 11). It is possible to specify a nominal photon beam energy which is different from the dose computation energy, for example to use a photon energy definition according to BJR #17.

The nominal energy will be displayed in the RayStation user interface, used in reports and as DICOM Nominal Beam Energy in both DICOM import and export.

The dose computation energy will be used for photon dose computation, including to get the correct GSTT parameters for dose computation with Varian Enhanced Dynamic wedge. It is therefore crucial to set a correct dose computation energy regardless of the selected energy definition. (149206)

WARNING!

Non-standard fluence mode. When modelling a photon beam quality with non-standard fluence mode (FFF/SRS), it is essential to select the correct fluence mode when adding the beam quality. If the fluence mode is not set correctly, plans using the beam quality may be misinterpreted by the LINAC, leading to incorrect delivered dose.

If standard fluence mode is used for the beam quality, RT Plans will set Fluence mode to "STANDARD" and the Fluence mode ID is not exported.

If non-standard fluence mode is selected, RT Plans will set Fluence mode to "NON_STANDARD" and the Fluence mode ID to the selected fluence mode (FFF/SRS). (508990)

Same nominal energy as the dose computation energy

For most users the nominal energy should be set to the same value as the dose computation energy. The RayStation photon dose computation internally uses a photon energy definition according to BJR #11 (British Journal of Radiology supplement number 11).When selecting to add a new photon beam quality, the default is to set the dose computation and nominal energies to the same value.

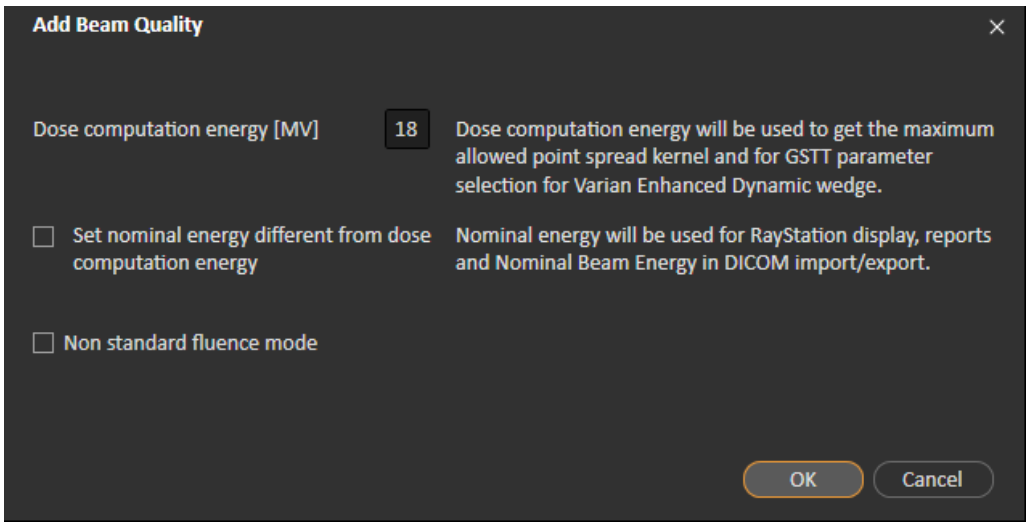

Add Beam Quality
Dose computation energy [MV]
18
Dose computation energy will be used to get the maximum allowed point spread kernel and for GSTT parameter selection for Varian Enhanced Dynamic wedge.
Set nominal energy different from dose computation energy
Nominal energy will be used for RayStation display, reports and Nominal Beam Energy in DICOM import/export.
Non standard fluence mode
OK
Cancel

Figure 16. The **Add Beam Quality** dialog for photons in the standard case where the nominal energy and the dose computation energy is set to the same value.

Different nominal energy than the dose computation energy

The main reason to use a nominal energy different from the dose computation energy is for users that use the BJR #17 energy definition. For such users, the relationship between nominal and dose computation energy usually is as follows:

Nominal energy [MV]	Dose computation energy [MV]
4	4
6	6
10	10
16	15
23	18
25	20

In the case that a nominal energy that is different from the dose computation energy is desired, check the checkbox **Set nominal energy different from dose computation energy**. It is then possible to enter a different value for the nominal energy.

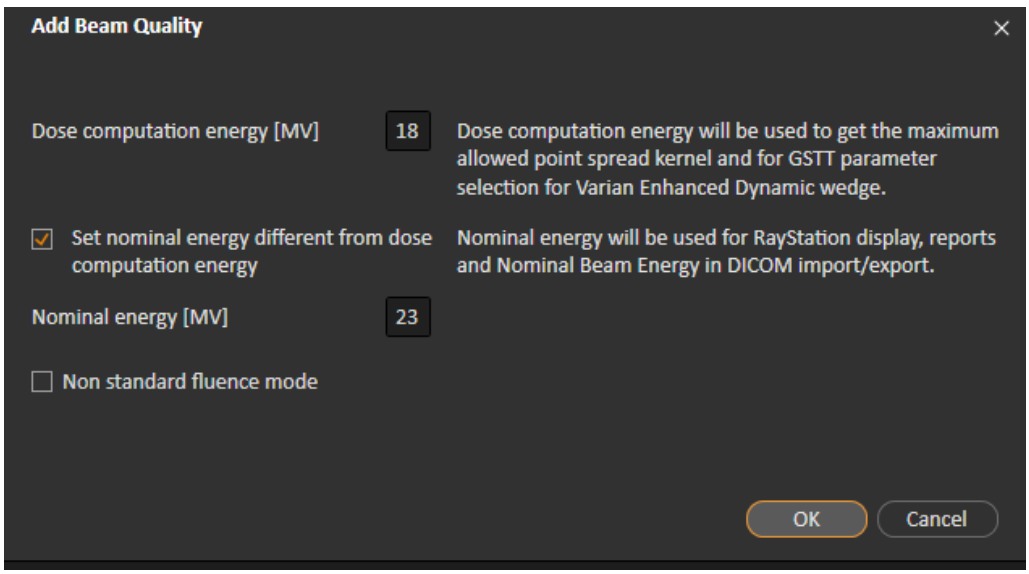
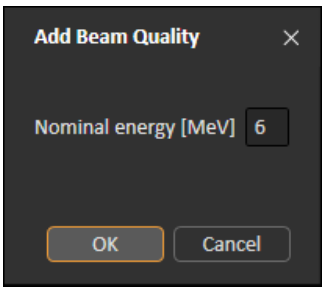

Add Beam Quality
Dose computation energy [MV]
18
Dose computation energy will be used to get the maximum allowed point spread kernel and for GSTT parameter selection for Varian Enhanced Dynamic wedge.
Set nominal energy different from dose computation energy
Nominal energy will be used for RayStation display, reports and Nominal Beam Energy in DICOM import/export.
Nominal energy [MV]
23
Non standard fluence mode
OK
Cancel

Figure 17. The **Add Beam Quality** dialog for photons in the rare case that a different nominal energy than the dose computation energy is entered.

3.4.2 Add electron beam quality

When adding an electron beam quality, nominal energy shall be specified and this energy is used throughout the system. Energies between 4 MeV and 25 MeV are supported. It is not possible to change the nominal energy after the beam quality has been added.



3.5 MACHINE CONSTRAINTS WORKSPACE

A machine is selected in the tree view by clicking the machine name. The right workspace will then show the machine constraints in a set of tabs. The machine constraints are used both when computing dose and optimizing plans.

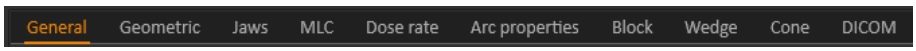


Figure 18. C-arm LINAC machine constraints. The contents of the tabs for C-arm LINAC machines are described in *section 4.2 Machine properties on page 110*.

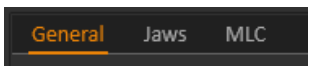


Figure 19. TomoTherapy LINAC machine constraints. The contents of the tabs for TomoTherapy LINAC machines are described in *section 5.2 Machine properties on page 227*.

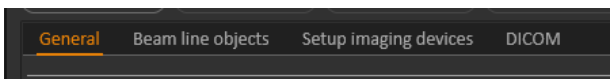


Figure 20. Ion treatment machine constraints. The contents of the tabs for Ion treatment machines are described in *section 6.1 Machine properties on page 248*.

3.6 PHOTON BEAM MODEL WORKSPACES FOR C-ARM LINACS

When a machine and a beam quality have been selected, the Beam Commissioning module shows an upper and a lower window.

The lower window shows the imported and computed dose curves and gives access to curve computation. The user can change **Output factors** and **Measurement conditions** by opening dialogs from here. **Curve quality** dialogs and **Auto Modeling** dialogs can also be reached from the lower window.

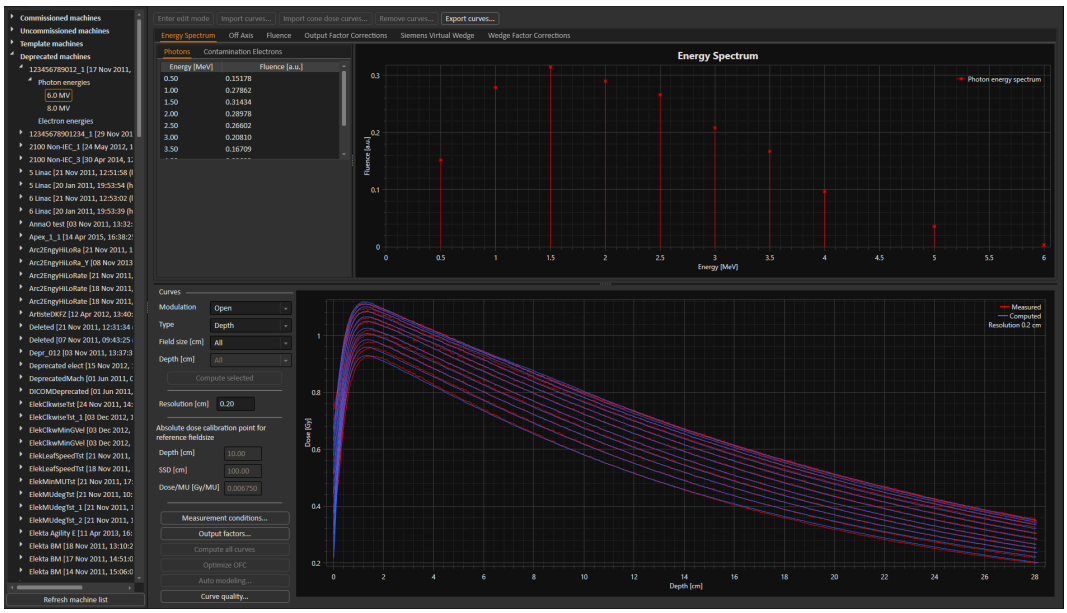


Figure 21. The Beam Commissioning workspace for a photon beam quality.

The upper window has different tabs containing parameters associated with different parts of the beam model for open fields. There are at least four beam model parameter tabs. For LINACs with Elekta Motorized Wedge, Siemens Virtual Wedge or Standard Wedges, there are two additional tabs for wedge parameters, there is one additional tab for LINACs with Varian Enhanced Dynamic Wedge and one additional for LINACs with cones.

Figure 22. The beam model parameter tabs for a machine with cones but no wedges.

The parameters in these tabs are used to compute the dose, both in the Beam Commissioning module and for patients. During the beam commissioning process, the parameters are adjusted such that the computations match measurement as closely as possible. The parameters are described further in *section 4.3 Beam model parameters for photons on page 141*.

3.6.1 Curve visualization

It is possible to choose which subset of curves should be visualized using the **Modulation** (Open, Wedge, Cones or None), **Type** (Depth, X, Y or Diagonal), **Field size** and **Depth** drop-down lists to the upper left in this sub-window. For a machine without imported wedged curves there will only be one modulation type (open) that can be selected. If there are wedged or cone curves it is possible to select two modulation types which are then visualized in different colors and line-styles. It is also possible to select only one type by choosing either the same modulation in both drop-down lists or by choosing Modulation=None in one of them. For diagonal profiles, the **Diagonal Position** is the radius of the measured point where the sign of the coordinate axis follows the direction of the imported measurement. If the curves have been recomputed using new parameter values, it is possible to select to **Display previous curves** by checking the corresponding checkbox.

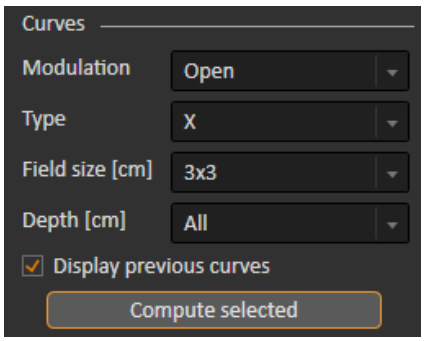


Figure 23. The curve visualization settings.

3.6.2 Curve labeling and colors

The measured curves selected in the first drop-down menu for modulation are red in the curve view and the corresponding computed curves are blue. The measured curves selected in the second drop-down menu for modulation are violet and dashed in the curve view and the corresponding computed curves are light blue and dashed. Previous computed curves are shown with dash-dot-dotted lines.

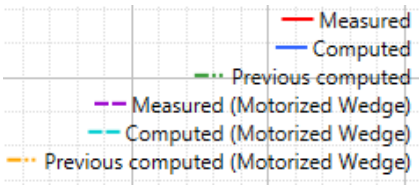


Figure 24. The curve presentation in the curve view.

3.6.3 Curve normalization

Measured depth dose curves are normalized so that the dose at the depth of the Absolute dose calibration point corresponds to a delivery of 100 MU. For the reference field size (*section 1.7.1 Reference point, reference field size and absolute calibration on page 23*), this dose is given by the Dose/MU field of the Absolute dose calibration point for the reference field size. For other field sizes, dose at the Absolute calibration point is scaled using the output factors (*section 4.1.4 Output factors on page 99*, *section 4.1.6 Absolute dose calibration point on page 105*). Measured profile dose curves are normalized so that the dose on the central axis corresponds to the dose of the the measured depth dose curve, for the same field size, at the depth of the profile.

If the x-profiles are measured with an offset from the central axis, the corresponding y-profiles are used instead of the depth dose curve in the normalization. The dose on the center of the profile will then be the same as the dose at the offset position on the y-profile.

3.7 PHOTON BEAM MODEL WORKSPACES FOR TOMOTHERAPY LINACS

When a machine and a beam quality have been selected, the Beam Commissioning module shows an upper and a lower window.

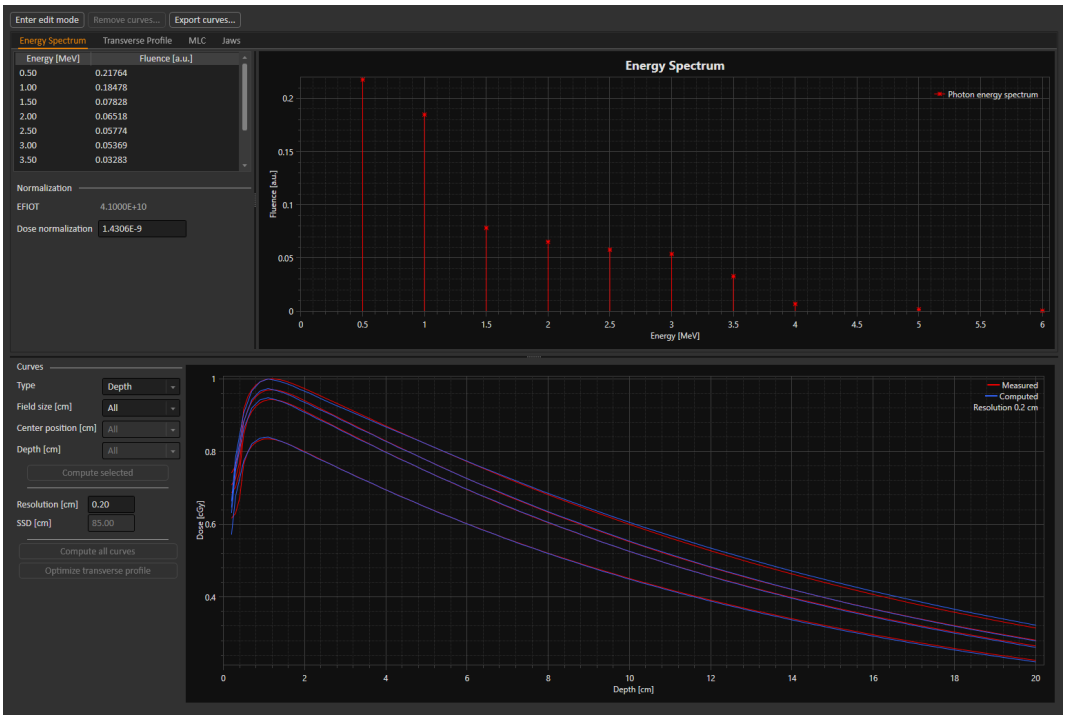


Figure 25. The Beam Commissioning workspace for a TomoTherapy beam quality.

There are four different tabs for a TomoTherapy beam quality, associated with different parts of the beam model.

Figure 26. The beam model parameter tabs for a TomoTherapy beam quality.

Depending on which tab has been selected, different information is shown in the upper and lower window. In the **Energy Spectrum** and **Transverse Profile** tabs, dose curves are shown in the lower window and beam model parameters in the upper window. In the **MLC** and **Jaws** tab, beam model parameters are shown in both the upper and lower window. The parameters in these tabs are used to compute dose, both in the Beam Commissioning module and for patients. The parameters are described further in *chapter 5 TomoTherapy LINAC treatment machines*.

3.7.1 Curve visualization

It is possible to choose which subset of curves should be visualized using the **Type** (Depth, X or Y), **Field size**, **Center position** and **Depth** drop-down lists to the upper left in the dose curve sub-window. The **Depth** drop-down list is only enabled for dose curve type X or Y and the **Center position** drop-down list is only enabled for dose curve type Y.

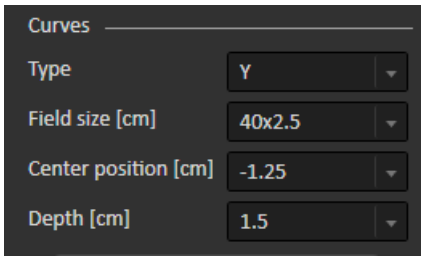


Figure 27. The curve visualization settings.

3.7.2 Curve labeling and colors

The measured curves are red in the curve view and the corresponding computed curves are blue.

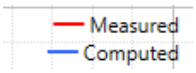


Figure 28. The curve presentation in the curve view.

3.7.3 Curve normalization

The measured dose curves have a relative normalization where the max dose of the largest field size is set to 1. The computed curves are individually normalized against the measured curves. For depth dose curves, the computed curves are normalized to the measured curves at a depth of 5 cm. For the profiles, the computed curves are normalized to the same maximum dose as the measured curves.

3.8 ELECTRON BEAM MODEL WORKSPACES FOR C-ARM LINACS

When a machine and a beam quality have been selected, the Beam Commissioning module shows an upper and a lower window.

The lower window shows the imported and computed dose curves and gives access to curve computation. The user can change **Output factors** and **Measurement conditions** by opening dialogs from here.

3.8.1 Workspaces for electron beam qualities

When an electron beam quality is selected in the machine tree view, the upper part of the workspace has the two tabs **Energy Spectrum** and **Source phase space**.

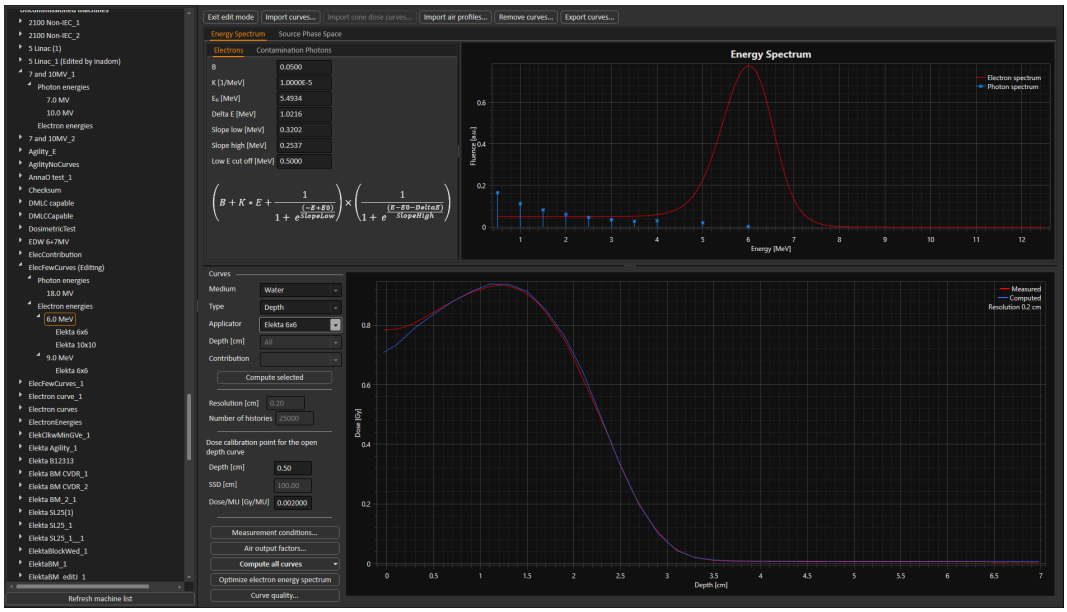


Figure 29. The electron beam quality workspace, showing the Energy Spectrum view.

In the **Energy Spectrum** view, the parameters for the electron energy spectrum can be edited. The resulting spectrum is shown as a red line in the plot. The energy spectrum of the contamination photons is shown as blue sticks. The shape of the contamination photon spectrum depends on E_0.

In the **Source phase space** view, the phase space parameters can be edited. The resulting radial fluence distribution and the dependence of the angular spread on radius are also shown.

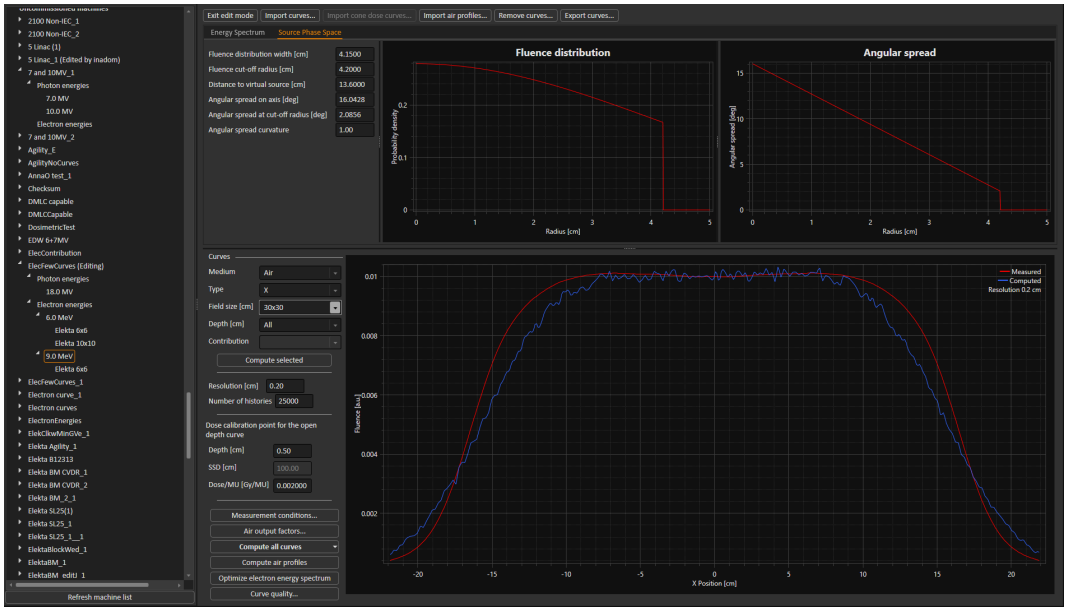


Figure 30. The electron beam quality workspace, showing the Source phase space view. In the lower sub-window, air profiles are selected for plotting.

The available commands differ slightly between an energy view and an applicator view. The **Measurement conditions** and **Curve quality** dialogs are available in both cases. The **Air output** factors dialog and the **Optimize electron energy spectrum** are only available for an electron energy.

Note that in order to use **Compute all curves**, the number of Monte Carlo histories must be set for all applicator curves. The property Number of histories shown in this view refers to the number of histories used for the air profile calculations.

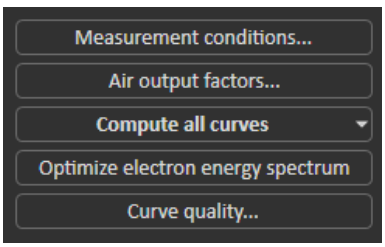
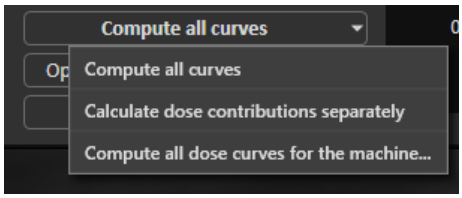


Figure 31. Commands available in the electron energy curve view.

When clicking the **Compute all curves** button, three options are available:


Compute all curves
Compute all curves
Calculate dose contributions separately
Compute all dose curves for the machine...

- The option **Compute all curves** calculates all air profiles and water dose curves for the selected beam quality.
- The option **Calculate dose contributions separately** is the same function as **Compute all curves**, but the different dose contributions (direct electrons, indirect electrons and photon contamination) are computed separately.
- The option **Compute all dose curves for the machine…** opens up the **Compute all electron dose curves and air profiles for the machine** dialog with a number of choices.

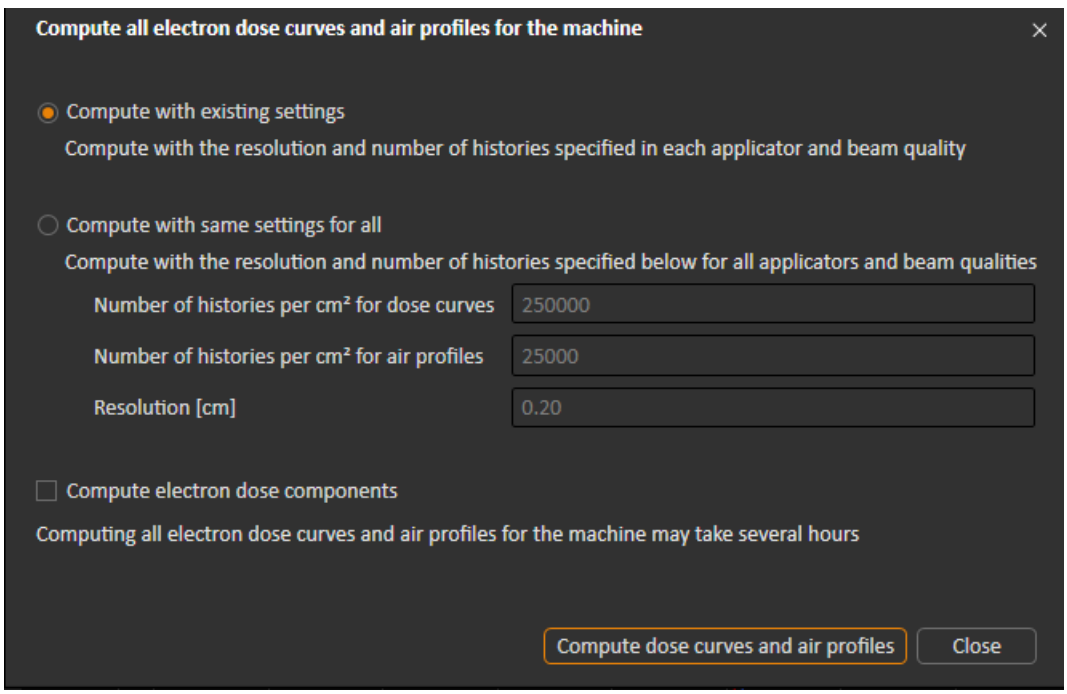

Compute all electron dose curves and air profiles for the machine
Compute with existing settings
Compute with the resolution and number of histories specified in each applicator and beam quality
Compute with same settings for all
Compute with the resolution and number of histories specified below for all applicators and beam qualities
Number of histories per cm² for dose curves
250000
Number of histories per cm² for air profiles
25000
Resolution [cm]
0.20
Compute electron dose components
Computing all electron dose curves and air profiles for the machine may take several hours
Compute dose curves and air profiles
Close

Figure 32. The Compute all electron dose curves and air profiles for the machine dialog.

It is possible to use the existing computation settings of each beam quality and applicator, then the **Compute with existing settings** radio button should be selected. This is selected by default.

If the same number of histories and resolution should be used for all beam qualities and applicators, select the **Compute with same settings for all** radio button and enter the desired settings in the fields below. The default settings are the ones required for commissioning of the machine.

It is also possible to compute the different dose contributions separately by checking the **Compute electron dose components** checkbox. Note that computing dose components separately will not allow commissioning of the machine.

Clicking the **Compute dose curves and air profiles** button will start a dose calculation for all electron dose curves for the selected machine.

3.8.2 Workspaces for applicators

When an applicator is selected in the machine tree view, the upper window has the three tabs **Electron applicator**, **Field shaping settings** and **Normalization**.

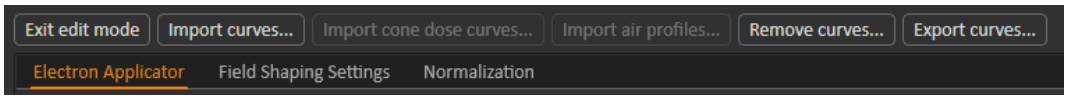


Figure 33. The electron beam model tabs for an applicator. Note that "cone" in the disabled button **Import cone dose curves** refers to photon cones. The button **Import air profiles** is enabled when an electron beam quality is selected in the machine tree view.

The lower sub-window looks the same as for an electron beam quality, but with fever options for curve display and a different selection of commands. Note that the size of the water phantom used for applicator dose curve computation is set under **Measurement conditions**.

Also note that the **Absolute dose calibration point** is given separately for each applicator, although the depth and SSD are typically the same for all applicators for a given energy. The dose calibration is not part of the beam model but simply normalizes the measured curves.

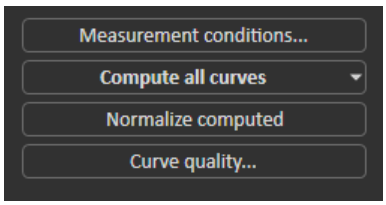
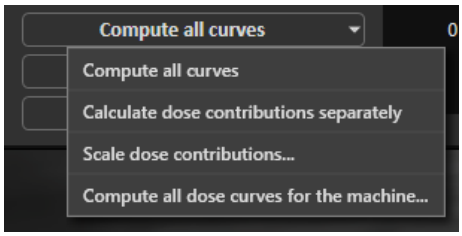


Figure 34. Commands available in the applicator curve view.

When clicking the **Compute all curves** button on the applicator level, four options are available:


Compute all curves
Compute all curves
Calculate dose contributions separately
Scale dose contributions...
Compute all dose curves for the machine...

- The option **Compute all curves** calculates all applicator curves for the selected beam quality.
- The option **Calculate dose contributions separately** is the same function as **Compute all curves**, but the different dose contributions (direct electrons, indirect electrons and photon contamination) are computed separately.
- The option **Scale dose contributions…** will open up the **Scale electron dose components** dialog where it is possible to scale the dose contributions for the selected applicator. This option is only available if the different dose contributions have been calculated.

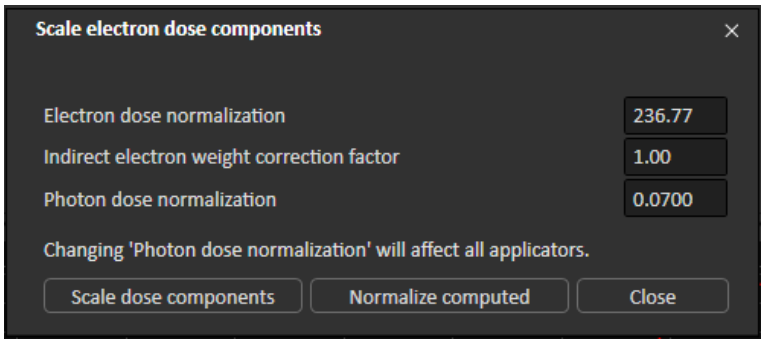


Figure 35. The Scale electron dose components dialog.

To rescale the dose contributions, change the desired weight in the **Scale electron dose components** dialog and click the **Scale dose components** button. Click the **Normalize computed** button to renormalize the computed curves against the measured curves.

- The option **Compute all dose curves for the machine…** opens up the same dialog as for the beam quality level.

3.8.3 Curve visualization

For an electron beam quality, it is possible to choose which subset of curves should be visualized using the **Medium** (Air or Water), **Type** (X or Y for Air and Depth, X or Y for Water), **Field size** or **Applicator** (depending on medium), **Depth** and **Contribution** (for Water only) drop-down lists to the upper left in this sub-window. If the curves have been recomputed using new parameter values, it is possible to select to **Display previous curves** by checking the corresponding checkbox. If an applicator is selected, the medium is always Water and some drop-down lists disappear.

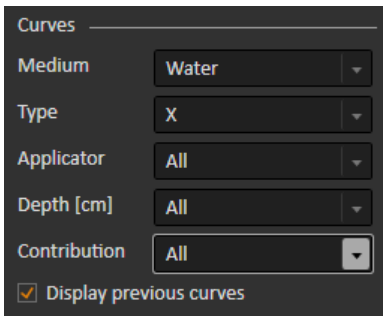


Figure 36. The curve visualization settings for an electron beam quality.

3.8.4 Curve labeling and colors

The measured curves are red in the curve view and the corresponding computed curves are blue. On the beam quality level, the Open depth dose curves are visualized with different line color, violet for measured and light blue for computed. Previous computed curves are shown with dash-dot-dotted lines. The direct electron contribution curve is shown as a dashed light blue line, the indirect contribution is shown as a dashed violet line and the photon contamination contribution is shown as a dashed dark orange line.

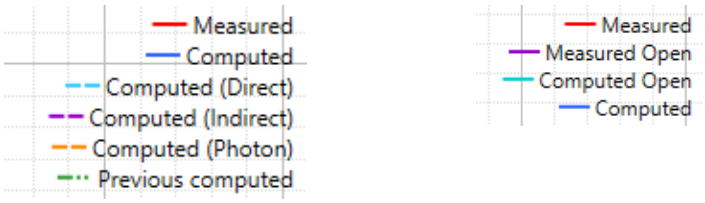


Figure 37. The curve graph legends in the curve view.

3.8.5 Curve normalization

Measured depth dose curves are normalized so that the dose at the depth of the Absolute dose calibration point (*section 1.7.1 Reference point, reference field size and absolute calibration on page 23*) corresponds to delivery of 100 MU. The Absolute dose calibration point is given separately for the open water depth curve and each of the applicator curves. Measured profile dose curves are normalized so that the dose on the central axis matches the dose of the corresponding measured depth dose curve, at the depth of the profile. Air profiles are normalized according to the Air output factors.

3.9 PROTON AND CARBON ION BEAM MODEL WORKSPACES

When a machine and a treatment technique have been selected, the Beam Commissioning module shows the machine parameters set during commissioning.

For treatment techniques PBS and Line Scanning the following workspaces are available: General, Scanning data, Spot profiles, Pristine Bragg peaks and Absoute dosimetry. For treatment techniques Uniform Scanning, Double Scattering and Wobbling the General workspace is available. For Mitsubishi Uniform Scanning machines, the Scanning data workspace is also available. The workspaces are described in *section 6.2 Beam quality parameters for Ion treatment machines on page 274*.

4 C-ARM LINAC TREATMENT MACHINES

This chapter describes the Beam Commissioning module for C-arm LINAC Treatment machines. This chapter contains information on how to enter measurement parameters, edit machine properties, edit beam model parameters and auto-modeling.

In this chapter

This chapter contains the following sections:

4.1	Enter measurements	p. 88
4.2	Machine properties	p. 110
4.3	Beam model parameters for photons	p. 141
4.4	Beam model parameters for electrons	p. 161
4.5	Applicator parameters for electrons	p. 166
4.6	Auto-modeling of photon beam model parameters	p. 171
4.7	Curve quality	p. 185
4.8	How to create a photon beam model	p. 191
4.9	How to create an electron beam model	p. 215

4.1 ENTER MEASUREMENTS

This chapter describes how measurements are deleted from and imported into the system and how measurement conditions are specified.

In this section

This section contains the following sub-sections:

4.1.1	Delete curves	p. 89
4.1.2	Import curves	p. 90
4.1.3	Export curves	p. 97
4.1.4	Output factors	p. 99
4.1.5	Measurement conditions	p. 101
4.1.6	Absolute dose calibration point	p. 105
4.1.7	Rectangular field interpretation	p. 106

4.1.1 Delete curves

To delete a curve:

1. Click the **Remove curves** button.

2. This opens the Remove curves dialog.

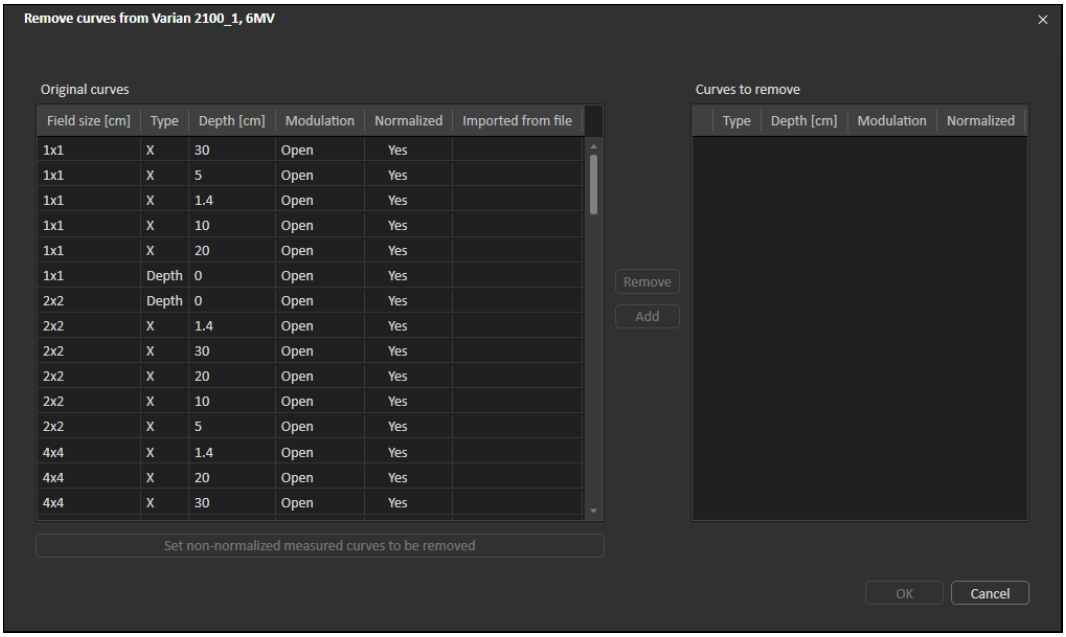

Remove curves from Varian 2100_1, 6MV
Original curves
Field size [cm] Type Depth [cm] Modulation Normalized Imported from file
1x1 X 30 Open Yes
1x1 X 5 Open Yes
1x1 X 1.4 Open Yes
1x1 X 10 Open Yes
1x1 X 20 Open Yes
1x1 Depth 0 Open Yes
2x2 Depth 0 Open Yes
2x2 X 1.4 Open Yes
2x2 X 30 Open Yes
2x2 X 20 Open Yes
2x2 X 10 Open Yes
2x2 X 5 Open Yes
4x4 X 1.4 Open Yes
4x4 X 20 Open Yes
4x4 X 30 Open Yes
Remove
Add
Curves to remove
Type Depth [cm] Modulation Normalized
Set non-normalized measured curves to be removed
OK
Cancel

Figure 38. The Remove curves dialog.

3. Select a curve in the list and click the **Remove** button.
4. Click **OK**.

If a depth dose curve is removed, all profiles of the same field size will be removed with it. If the reference field depth dose curve is removed, all fields will be removed with it. The reason is that the reference field depth dose curve is used to normalize all other curves, and the depth dose curve for each field size is used to normalize the profiles.

4.1.2 Import curves

To import curves the correct beam quality and/or applicator must be selected. The energy and the modality must correspond to the selected beam quality.

Import curves by clicking the **Import curves** button. The file formats *.csv, *.mcc, *.asc/rfa, *.snctxt and *.xmcdat are supported. All formats except *.xmcdat can be opened and reviewed in a text editor. These text formats and the interpretation of the files are described in detail in *Appendix B Dose curve format*. The .xmcdat files cannot be opened in a text editor for review, but are expected to be correctly exported and hence correctly imported into RayPhysics.

WARNING!

Beam model quality depends on beam data. The quality of the beam model depends critically on the quality and scope of the beam data, for example, dose curves, output and wedge factors, absolute calibration, phantom size and collimation settings which influence the curve field setup. The entered measurement conditions must match the measurement technique. The sizes of the measured fields should cover the field sizes of the future applications of the beam model.

All input data, such as measured curves and output factors, must be coherent and correspond to the delivery system which is to be commissioned. Otherwise the generated beam model will not be able to calculate a correct dose.

For more information, refer to the *RSL-D-RS-9A-BCDS, RayStation 9A Beam Commissioning Data Specification*. (508979)

WARNING!

Always review curves after import. Always review curves after import to ensure consistency with the measurement situation. The beam model quality depends critically on correctness of the imported data. (508984)

Import photon curves

The curves must be measured with the same SSD as the absolute calibration point. To remove curves from the import, select the curves in the **Curves to import list** and click the **Remove** button.

The next step of the import procedure is to specify output factors (*section 4.1.4 Output factors on page 99*) and measurement conditions (*section 4.1.5 Measurement conditions on page 101*). Curves cannot be imported without output factor and detector size specification. Note that these values can be edited at any time after the curves are imported.

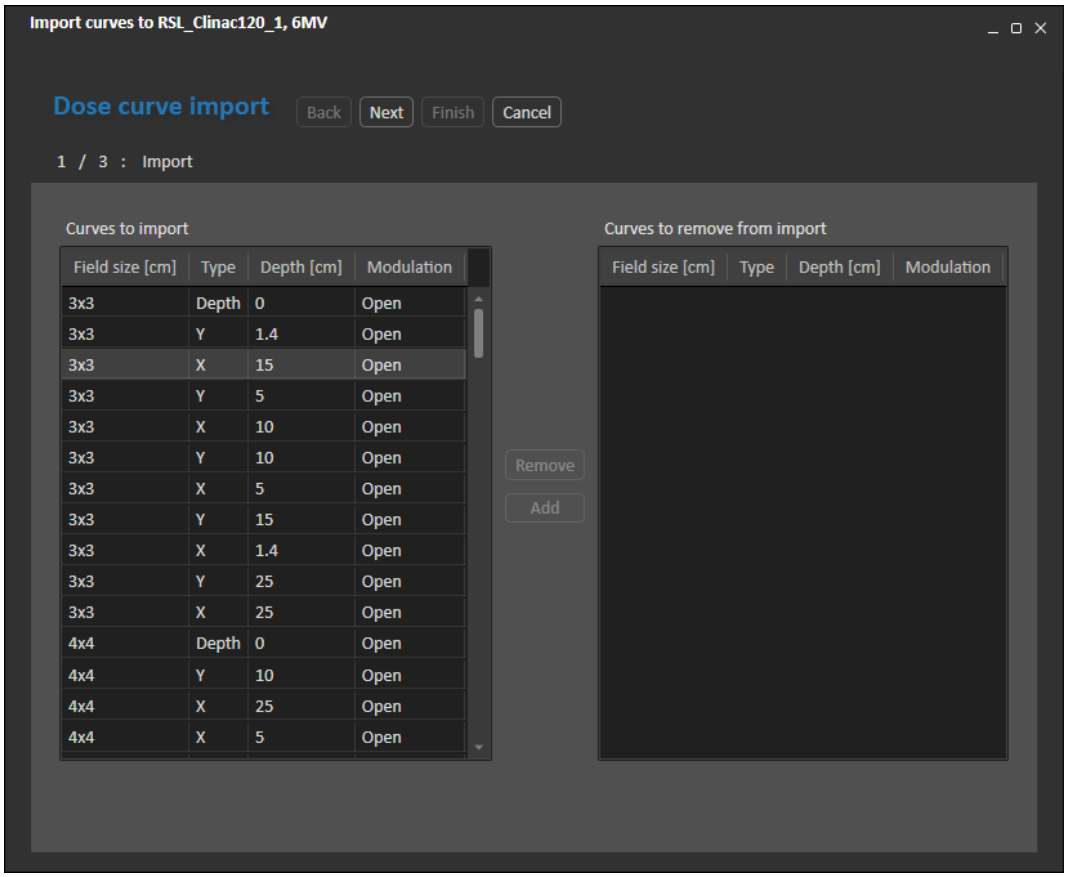


Figure 39. The Import curves dialog.

Note: *When importing curves on the *.xmcdat format, there may be curves with different SSD in the file. The curves with SSD corresponding to the SSD of the absolute calibration point will be imported, curves with another SSD will be ignored. Make sure that the SSD of the absolute calibration point correspond to the SSD of the curves that you want to import.*

Import wedged curves

The workflow is to first import the open curves, then the wedged curves wedge angle by wedge angle. The curves are automatically scanned to find the wedge orientation; all curves for one wedge angle must have the same orientation. The wedge angle and orientation must be allowed to allow curve import (*Allowed wedges on page 135*). If it is not possible to find the wedge orientation based on the measured curves, the user will be prompted to enter the correct orientation.

For machines with Elekta Motorized Wedges, the model must be tuned for the 60 degrees wedge angle and therefore the fully wedged curves must be imported before commissioning.

For Standard Wedges there is one wedge model per enabled wedge angle; for each wedge angle the wedged dose curves must be imported and computed before commissioning.

For machines with Siemens virtual or Varian Enhanced Dynamic wedges, it is possible to only import profile curves and instead copy the open PDD and use also for the wedge curves.

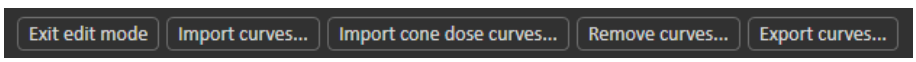
WARNING!

Dose curve wedge orientation. The wedge orientation for wedged curves is determined from the curve at import. All wedge angles must have been measured with the same orientation. If all curves do not have the same wedge orientation, then no curves will be imported. For curves where the orientation cannot be determined, it is assumed to be identical to other curves imported at the same time. (508987)

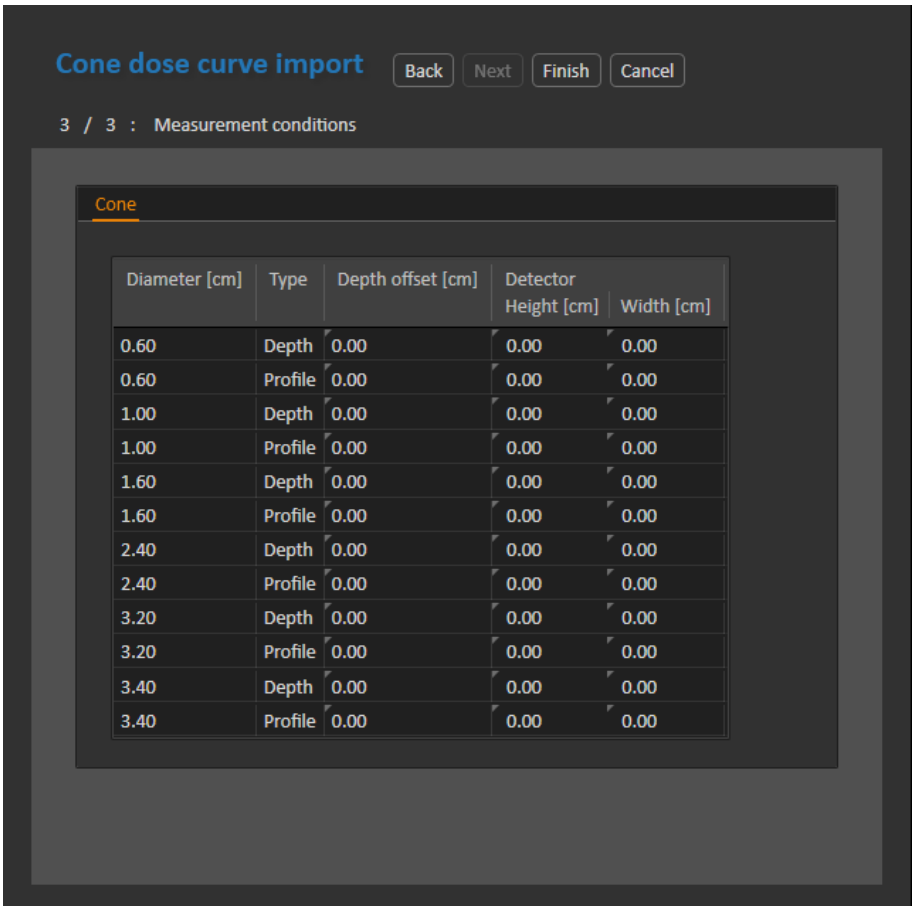
Note: *The recommended workflow is to finish the beam modeling for the open fields first and only after that add wedges to the model. This will speed up the Compute all dose curves option since the wedged curves do not need to be computed when working on the open field curves.*

Import cone curves

To import cone curves, click the **Import cone dose curves...** button.



The field size property in the dose curve files will be read as cone diameter. It is not possible to import cone curves where the field size in the file does not match the diameter of any cone specified for the beam quality. For *.csv files, a ConeName property has been added, files with this property will only be possible to import as cone curves and this property is mandatory in files that are imported as cone curves. Selecting to import cone curves will start the same wizard as for open curves. It is not possible to import diagonal curves for cones.



Diameter [cm]	Type	Depth offset [cm]	Detector Height [cm]	Width [cm]
0.60	Depth	0.00	0.00	0.00
0.60	Profile	0.00	0.00	0.00
1.00	Depth	0.00	0.00	0.00
1.00	Profile	0.00	0.00	0.00
1.60	Depth	0.00	0.00	0.00
1.60	Profile	0.00	0.00	0.00
2.40	Depth	0.00	0.00	0.00
2.40	Profile	0.00	0.00	0.00
3.20	Depth	0.00	0.00	0.00
3.20	Profile	0.00	0.00	0.00
3.40	Depth	0.00	0.00	0.00
3.40	Profile	0.00	0.00	0.00

The measurement conditions for cones only include depth offset and detector sizes. No field collimation, since the collimators will be positioned according to the specification for the cone.

Import electron curves

Import open water depth curves or applicator curves

1. Select the correct beam quality to import the open water depth curve or applicator respectively in the machine tree.

   It is not possible to import all applicator curves at once.

2. Click the **Import curves…** button.
3. Remove any unwanted files from the **Curves to import** list and continue.
4. Specify the phantom size and depth offset in the **Measurement conditions** dialog.

   For more information about measurement conditions, see *section 4.1.5 Measurement conditions on page 101*. For a LINAC with an MLC narrower than 40 cm, the field collimation for

the open water depth curve should be set to "Jaws only collimated", otherwise curve calculation will not be possible.

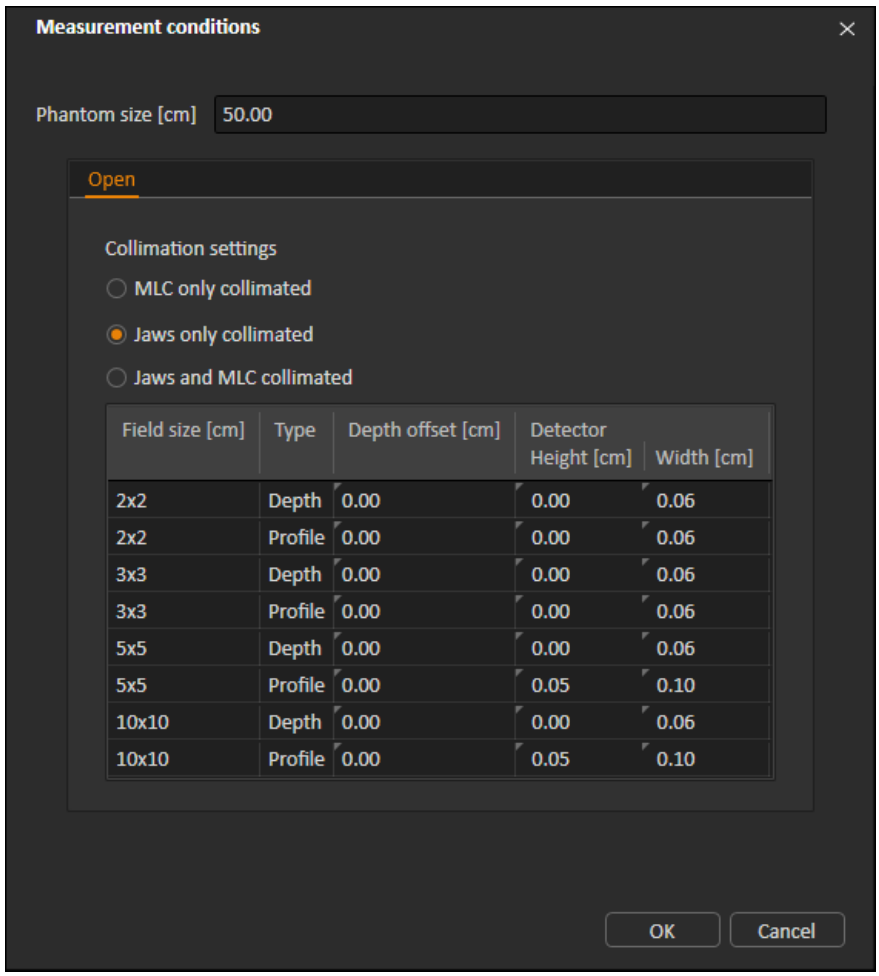


Figure 40. The Measurement conditions dialog for photon curves.

Import air profiles

1. Select the correct beam quality and click the **Import air profiles…** button.
2. Remove any unwanted files from the **Curves to import list** and continue.
3. Enter the air output factors in the **Output Factors** dialog.

Note: *The open water depth dose curve must be imported to allow import of air profiles.*

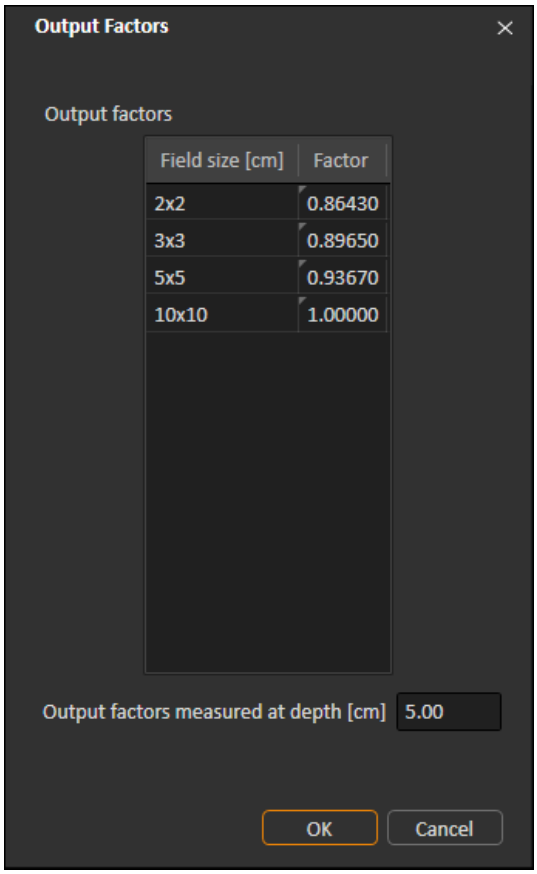


Figure 41. The Output Factors dialog.

For more information, see *RSL-D-RS-9A-BCDS, RayStation 9A Beam Commissioning Data Specification*.

Centering of dose curves

A good beam model relies on good input data. Ensure that the phantom measurements are performed so that the profiles are centered on the origin. Still, if the profiles are shifted by less than 1 cm, each profile is auto-centered at curve import. Wedged profiles are not centered, since the maximum gradient centering did not improve field centering for well aligned profiles. Ensure that the dose curves are centered before entering them into RayStation. In RayStation 4.7 and previous versions, wedged profiles were centered. When copying an old model which had centered measured dose curves the centering will be removed, and you may find alignment differences at recomputation. Open fields are centered using the coordinates at FWHM (full width at half maximum). If data processing is needed, this should be done before the profiles are imported into RayPhysics 9A. This includes data smoothing.

Note: *The centering of the dose curves is automatic and cannot be affected by the user. No information is given that a curve has been automatically centered.*

Note: *The centering of the dose curves will be less accurate if the distance between measured dose points is large since the edge of the field will depend on the position of the measured data points. If the imported curves have been interpolated before import, the quality of the interpolation will also influence the quality of the auto centering.*

Note: *If a measured curve seems shifted with respect to the central axis and to the computed curve, this may be caused by a faulty auto centering. It is not possible to influence the auto centering procedure directly, although the curve may be smoothed or resampled and then re-imported.*

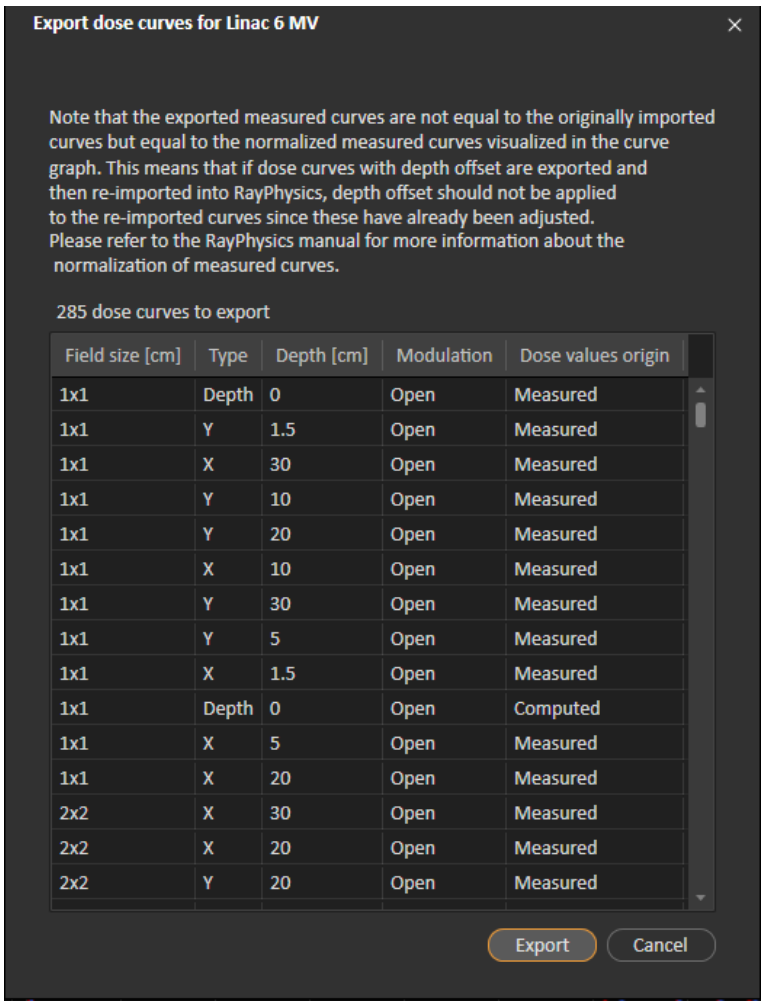
4.1.3 Export curves

All measured and computed curves for a selected beam quality can be exported to the csv format. See *Appendix B Dose curve format* for information about the format.

To export all curves for a selected beam quality:

1. Click the **Export curves** button.

   This opens a dialog showing all dose curves that are possible to export.


Export dose curves for Linac 6 MV
Note that the exported measured curves are not equal to the originally imported curves but equal to the normalized measured curves visualized in the curve graph. This means that if dose curves with depth offset are exported and then re-imported into RayPhysics, depth offset should not be applied to the re-imported curves since these have already been adjusted. Please refer to the RayPhysics manual for more information about the normalization of measured curves.
285 dose curves to export
Field size [cm] Type Depth [cm] Modulation Dose values origin
1x1 Depth 0 Open Measured
1x1 Y 1.5 Open Measured
1x1 X 30 Open Measured
1x1 Y 10 Open Measured
1x1 Y 20 Open Measured
1x1 X 10 Open Measured
1x1 Y 30 Open Measured
1x1 Y 5 Open Measured
1x1 X 1.5 Open Measured
1x1 Depth 0 Open Computed
1x1 X 5 Open Measured
1x1 X 20 Open Measured
2x2 X 30 Open Measured
2x2 X 20 Open Measured
2x2 Y 20 Open Measured
Export
Cancel

2. Select **Export** to export the curves.

   This opens the Browse for folder dialog.

3. Specify a location for the exported dose curves.

4. Click **OK**.

For photon beam qualities, open, wedged and cone curves are exported separately. For electron beam qualities, air profiles and the open depth dose curve will be exported separately when a beam quality level is selected. Applicator curves are exported from the applicator level. Measured and computed curves (if available) are exported into separate files.

The measured curve data that is exported is not equal to the originally imported curve data. Instead, the exported measured curves are normalized (described in *section 3.8.5 Curve normalization on page 84*) and adjusted with depth offset (see *Depth offset on page 102*) and for profiles also centered (see *Centering of dose curves on page 95*). The reason for exporting normalized and adjusted measured curves is so that they match the computed curves if the beam model has been adjusted to the measured curves. This makes it possible to compare exported measured and computed dose curves in an external tool, since they match in positions and dose normalization. The exported normalized measured curves are equal to the measured curves visualized in the curve graph. It is not possible to export the original measured curve data. Note that this means that if dose curves with depth offset are exported and the re-imported into RayPhysics, depth offset should not be applied to the re-imported curves since these have already been adjusted.

Note: *The csv dose curve export in RayPhysics does not take MLC and Jaw field size into account. When exporting dose curves for a machine where MLC and Jaw field size have been set for the measured curves, this information will be ignored and only the nominal field size will be exported. If re-importing exported dose curves into RayPhysics, the information about MLC and Jaw field size will be lost.*

4.1.4 Output factors

The Output factors dialog can be opened by clicking the **Output factors** button. It is also opened automatically when importing dose curves. The Output factors dialog is used to enter measured normalization information for different field sizes.

Note: *The output factors only influence the measured dose curve normalization. They are NOT part of the beam model which is used to compute dose in patient or in Beam Commissioning.*

Open field output factors

There should be output factors entered only for field sizes for which scans have been imported. The output factors must be measured with the same SSD as the absolute calibration point and the curves. The reference field size (*section 1.7.1 Reference point, reference field size and absolute calibration on page 23*) used for the absolute calibration must have the output factor value 1. For field sizes smaller than the reference field size the output factors will be smaller than 1. For field sizes larger than the reference field size the output factors will be larger than 1.

The output factors set the absolute dose level for the measured curves which are shown in the curve interface and used for auto-modeling. The visualized reference field is scaled to 100 MU using the dose in the absolute calibration point. Other field sizes are scaled such that the dose at the output factor depth corresponds to the dose in the same point for the reference field size times the output factor. Measured profiles are scaled so that the dose on the central axis matches the dose of the corresponding measured depth curve, at the depth of the profile.

Note: *Reference field size output factor. The output factor of the reference field size should always be 1.*

Note: *The output factor depth must correspond to the depth used at measurement. If this is not the case, a comparison between computed and measured curves may not reflect the best model possible.*

Wedge output factors

The wedge output factor for a field size is defined as the dose for the wedged field at a specified depth on the central axis divided by the dose for the same size open field at the same depth. The wedge output factors must be measured with the same SSD as the absolute calibration point and at the same depth as the output factors.

If there are wedged curves for field sizes without corresponding open curves, the field sizes appear automatically in the output factor table. Complete the table with the output factors for the open fields. There should be wedge output factors only for imported field sizes.

The wedge output factors set the absolute dose level for the measured wedged curves. Thus the dose at the output factor depth corresponding to the wedged curve is the same as the dose at the same point for the corresponding open field times the wedge output factor.

Siemens virtual wedges are calibrated to give the same output for wedged and open fields on the central axis. If entering wedge output factors for the Siemens virtual wedge these should be close to one.

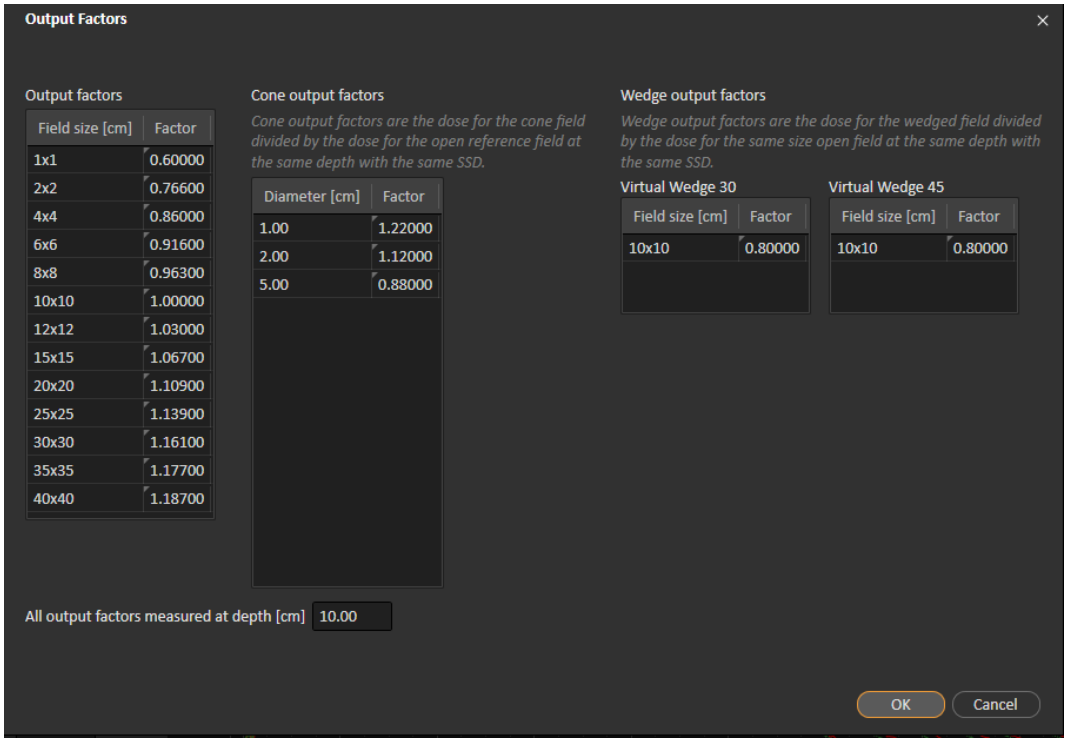

Output Factors
Output factors
Field size [cm] Factor
1x1 0.60000
2x2 0.76600
4x4 0.86000
6x6 0.91600
8x8 0.96300
10x10 1.00000
12x12 1.03000
15x15 1.06700
20x20 1.10900
25x25 1.13900
30x30 1.16100
35x35 1.17700
40x40 1.18700
Cone output factors
Cone output factors are the dose for the cone field divided by the dose for the open reference field at the same depth with the same SSD.
Diameter [cm] Factor
1.00 1.22000
2.00 1.12000
5.00 0.88000
Wedge output factors
Wedge output factors are the dose for the wedged field divided by the dose for the same size open field at the same depth with the same SSD.
Virtual Wedge 30
Field size [cm] Factor
10x10 0.80000
Virtual Wedge 45
Field size [cm] Factor
10x10 0.80000
All output factors measured at depth [cm] 10.00
OK
Cancel

Figure 42. The **Output Factors** dialog showing wedge output factors.

Cone output factors

The cone output factors are relative to the open reference field size. Cone output factors must be entered for all cone sizes specified for the machine, and must be measured with the same SSD and at the same depth as the open output factors.

4.1.5 Measurement conditions

The Measurement conditions dialog can be opened by clicking the **Measurement conditions...** button. It is also opened automatically when importing dose curves. The Measurement conditions dialog describes the conditions during curve measurement. The measurement conditions have one thing in common: they influence the dose curve computation during beam commissioning but they are not part of the beam model which is used to compute dose in the patient.

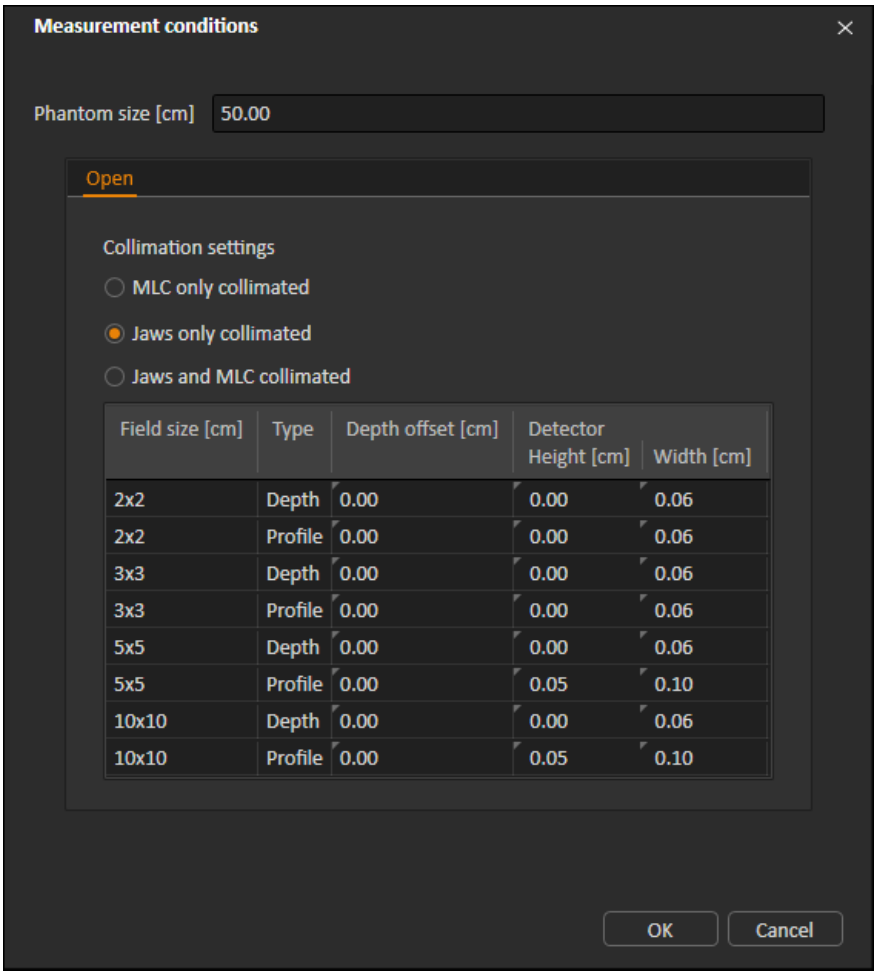


Figure 43. The **Measurement conditions** dialog.

Phantom size

The phantom size value should match the measurement conditions as closely as possible. A cubic water phantom where each side has the size of the phantom size is used for dose curve computation. A computation phantom size which is smaller than the measurement phantom would give a

computation with too little backscatter. During modeling this would then be compensated for with model changes. The model changes would in turn lead to overestimation of dose.

When entering the phantom size, it may be suitable to enter a size that will ensure that the curves are calculated in the center of the TERMA grid voxels instead of at the edge between the voxels. To achieve this, enter a phantom size that gives an uneven integer when divided with the resolution. For example, if the phantom size was 10 cm at measurement and the resolution is 1 cm, enter a phantom size of 11 cm to get the center of a voxel on the central axis. The difference between calculating in the voxel center and the voxel edge is usually less than 0.5%. For more information see *section 4.8.3 Resolution on page 194*.

The same phantom size is used for computation of all dose curves. The phantom size can be changed during the commissioning progress.

Detector sizes for photon curves

If the measured curves have not been de-convolved to account for detector size smearing before import to the Beam Commissioning module, a detector width and height which best approximates the specific detector used to measure the curves should be set. If several fields use the same detector, enter values for one field size, mark the other field sizes and right-click to select copying of values between field sizes.

The implemented detector smearing is a rectangular box square well, i.e. the smearing function is constant inside the box and zero outside. The detector height parameter mainly influences the computed dose curve in the build-up region and the detector width parameter mainly affects the profile penumbra. Detector size is specified per field size, per depth dose curve/profiles and for open/wedged/cone curves. See the *RSL-D-RS-9A-RCF, RayStation 9A Reference Manual* for computation details.

For an ionization chamber the corresponding square well height and width is generally slightly smaller than the physical detector height and width.

Note: *The detector smearing is used for all points along the computed curves. To match the measured and computed dose curves, the size of the detector used to measure the output factors should be similar in size to the detector used to measure the curves for the corresponding field size. The detector used to measure the absolute calibration should match the detector used to measure the curves for the reference field size.*

Note: *A large detector size will also smoothen the computed curves. The computed curves are generally smooth to start with, the exception being the electron bump in the build-up region described in problem 7 in section section 4.8.8 Common problems and solutions on page 211. A large detector height may therefore mask a sub-optimal electron model. If the bump is large enough, it will however be seen also with a large detector height.*

Depth offset

A depth offset can be applied to the depth of all measured depth dose curves and profiles. A positive depth offset shifts the measured curves towards larger depths. The offset is applied before

normalization of measured curves using the calibration point and the output factor measurement point. This means that it is assumed that the measured curves are offset, but the calibration point and the output factor point are corrected for the effective point of measurement. The effective point of measurement for an ionization detector is generally at 1/3 of the detector diameter from the upper surface. If the calibration point and the output factor point are not corrected for the effective point of measurement, add the corresponding shift to the depth of the calibration point and the depth of the output factor point. The depth offset is specified per field size, per depth dose curve/profiles and for open/wedged/cone curves.

Collimation settings for photon curves

The collimation specifies how the fields for the measured curves were collimated. Collimation must be rectangular and symmetric around the x-axis and the y-axis. There are three possible collimation settings:

- **MLC only collimated**: The MLC is positioned at the nominal field size and the jaws are retracted. Selecting this option results in two additional columns:
  - **Jaw field size**: The field size to which the jaws are retracted. See *section 4.1.7 Rectangular field interpretation on page 106*
  - **MLC leaf tip offset**: The position of the closed MLC leaf tips as an offset compared to the central axis. Not used for fixed jaw machines. See *section 4.1.7 Rectangular field interpretation on page 106*

  Note: *The jaw field size and MLC leaf tip offset parameters are set per field size, and it is also possible to set per depth dose curve/profiles. However, it is strongly recommended to have the same values for the depth dose curve/profiles to get the same output for both depth dose curves and profiles.*

  Note: *For a machine with the jaws closer to the source than the MLC, for example Varian LINACs, the field measure is calculated from the jaws also when the MLC only collimated option is selected. This means that the same output factor correction will be used for all MLC only collimated fields with the same jaw field size and the related output factor correction will be for the jaw field size and not the nominal field size. For these machines, it is recommended to only retract the jaws a little from the MLC if MLC only collimated fields are to be used. Refer to the RSL-D-RS-9A-REF, RayStation 9A Reference Manual for information on the field measure calculation.*
- **Jaws only collimated**: The jaws are positioned at the nominal field size and the MLC is retracted to ± the **Maximum tip position** set in the **MLC** tab.
- **Jaws and MLC collimated**: Both MLC and jaws are positioned at the nominal field size.

It is allowed to measure the x-profiles with a small offset in the y direction for MLC only collimated and Jaws and MLC collimated fields in order to avoid measuring the profile in the tongue-and-groove region. This parameter is called **x-profile offset** and is read from the measured curves. The x-profile offset has to be the same for all x-profiles.

For curves that have been imported on the *.xmcdat format, both MLC and jaw field size is read from the file. The nominal field size is set to the minimum opening of the MLC and jaws. It is not possible to select another field collimation.

4.1.6 Absolute dose calibration point

The Absolute dose calibration point is given for the reference field size for photons. For electrons, it is given separately for open water measurements and each of the applicators. In the **Absolute dose calibration point for reference field size** box, enter the depth in cm, the SSD in cm and the dose to MU conversion (cGy/MU or Gy/MU depending on the settings in RayPhysics 9A) for your absolute calibration point. This value will be used to set the dose level of the measured reference curves.

Note: *The absolute calibration is not used for dose computation, neither for dose curves nor in the planning mode. The dose level of the dose computation is instead set by the beam model parameters.*

Note: *If the SSD entered in the Absolute dose calibration point for reference field size box differs from the SSD of the measured curves, the Beam Commissioning module will not import the curves. SSD can only be edited at the stage when the machine has no curves.*

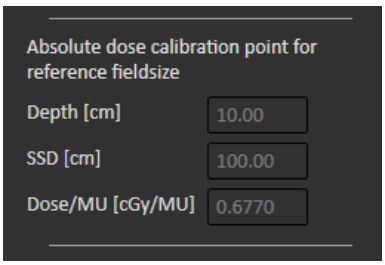


Figure 44. The photon Absolute dose calibration point for reference field size.

4.1.7 Rectangular field interpretation

The collimation for rectangular fields used when computing curves during beam commissioning depends on the collimator settings and the position of the collimators along the axis from source to isocenter. If the MLC leaves were actually retracted at the measurement, select collimation setting **Jaws only collimated**. This will put the leaves at ± the **Maximum tip position** set in the **MLC** tab. If **MLC only collimated** is selected, the MLC is put at the nominal field position and dose can only be computed for fields which are consistent with the MLC leaf boundaries. The MLC will conform to the field size in x, if the collimation setting **Jaws and MLC collimated** has been selected (*Collimation settings for photon curves on page 103*). The y direction is handled differently dependent of the machine type, see the following sections for more information.

For a machine with MLC type set to Y, the x and y directions are interchanged. That is, the MLC will conform to the field size in y if for example **Jaws and MLC collimated** has been selected.

Fixed jaw machines

For fixed jaw machines, the jaws are positioned at the values set in the jaw tab. The MLC is put at the exact position of the rectangular field border and dose curves can only be computed for fields which are consistent with the leaf positions. Closed leaf-pairs are parked at a distance of the minimum leaf/jaw overlap behind the x-jaw border. This is also done for collimation setting **MLC only collimated**, which means that **MLC leaf tip offset** is not used for machines with fixed jaws.

Dual-layer MLC

For machines with dual-layer MLC, both MLC layers are used to collimate the field. One layer must be put at the exact position of the rectangular field border and dose curves can only be computed for fields that are consistent with the leaf positions.

Y-jaw is closer to the isocenter than the MLC is

For machines where the y-jaw is closer to the isocenter than the MLC is, the y-jaw is put at the field border. All MLC leaves which would shadow the opening are opened. In addition to this, the MLC leaves which have their inner border in line with the y-jaw are opened; they are then put to the x-jaw position. Also a leaf which has its innermost border positioned at less than 1% of the leaf width inside the jaw is opened. This is the automatic behavior of MOSAIQ with Elekta (not Elekta Beam Modulator) in service mode. Make sure that this is the actual behavior when measuring curves, output factors and absolute calibration.

MLC is closer to the isocenter

For machines where the MLC is closer to the isocenter than the jaws are, both the MLC and the jaws are put at the field border. Leaves which are covered by the y-jaw are put on the central axis and at the minimum static gap, even if this means that machine constraints are not fulfilled.

Note: *It is important that the field setup used when measuring dose curves matches the field setup used in beam commissioning. If this is not the case, a comparison between computed and measured curves may not reflect the best model possible since the internal representation of the jaws and MLC leaves are not correct.*

The following images illustrates how rectangular fields are interpreted internally in Beam Commissioning.

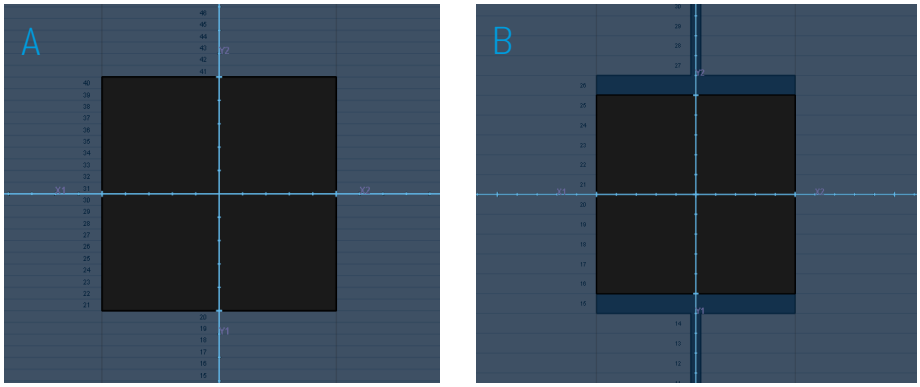


Figure 45. A) Both MLC and jaws for a Varian machine where the MLC is the primary collimator, i.e. the jaw is closer to the primary source than the MLC is.
B) Both MLC and jaws for an Elekta machine where the jaw is the primary collimator, i.e. the MLC is closer to the primary source than the y-jaw is.

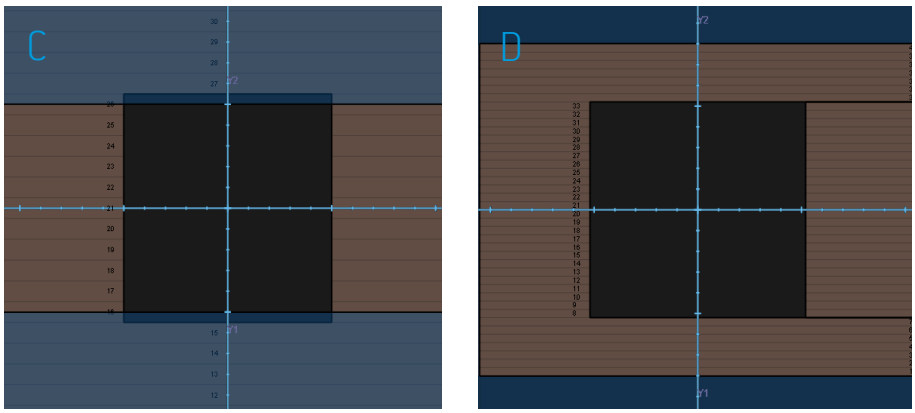


Figure 46. C) Both MLC and jaws for a machine without backup jaw.
D) Both MLC and jaws for a machine with fixed jaws.

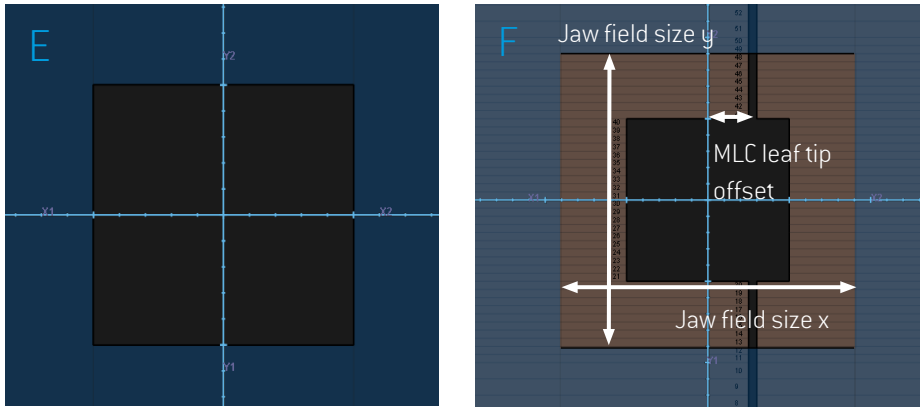


Figure 47. E) Only jaws.
F) Only MLC.

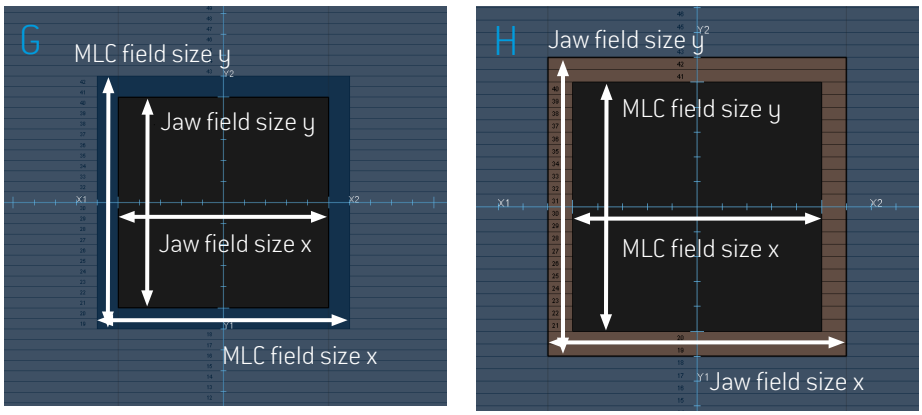


Figure 48. G) Jaw is main collimator for curves imported on the .xmcdat format. Nominal field size is given by the jaw opening.
H) MLC is main collimator for curves imported on the .xmcdat format. Nominal field size is given by the MLC opening.

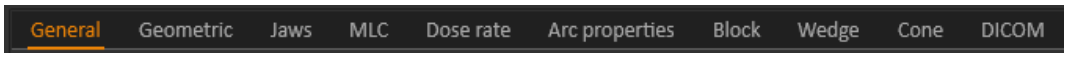
Machines without backup jaw

For machines without backup jaw, the Jaws only collimated option is not available. For the Jaws and MLC collimated option, the jaw is put at the field border. The MLC will be put at the field border in the x direction. For machines where the y-jaw is closer to the isocenter, an extra leaf pair will be opened in the y direction in the same way as described in section . For machines where the MLC is closer to the isocenter, the MLC will be put as close as possible to the field border in the y direction (depending on the field size and the MLC leaf width). The MLC opening in the y direction will always be larger than the field size if it is not possible to put it at the field border.

Note: *The circular primary collimator that may limit the diagonal field size is not taken into account in the RayPhysics field setup. Neither are the Elekta corner leaves.*

4.2 MACHINE PROPERTIES

This chapter describes the machine properties which define the limits of what the machine can deliver. The parameters are shown in the right window when clicking on the machine name in the machine tree view. In the right window there are a number of tabs containing the different machine properties. The **Arc properties** tab is only visible for machines that are Static arc or VMAT and Conformal Arc capable. The content of each tab is described in this chapter.



In this section

This section contains the following sub-sections:

4.2.1	General properties	p. 112
4.2.2	Geometric properties	p. 117
4.2.3	Jaw properties	p. 119
4.2.4	MLC properties	p. 122
4.2.5	Dose rate properties	p. 126
4.2.6	Arc properties	p. 129
4.2.7	Block properties	p. 133
4.2.8	Wedge properties	p. 134
4.2.9	Cone properties	p. 137
4.2.10	DICOM	p. 139

Precautions

WARNING!

Machine constraints. If the machine constraints defined in RayPhysics do not reflect the treatment machine and R&V-system behavior, the plans can either be stopped at delivery or adjusted outside RayStation giving a situation where the delivered dose differs from the approved dose. When creating a machine model from a template, ensure that all machine constraint parameters are adapted to your specific treatment machine.

Even if RayStation adheres to all machine constraints specified in RayStation, there is no guarantee that all plans will be possible to deliver. Ensure that plans are not modified outside RayStation in a way that significantly affects dose without proper evaluation. (508980)

Note: *Special care should be taken when specifying the jaw and MLC constraints for a machine with an add-on MLC. For a LINAC equipped with an add-on MLC, such as for instance the m3 from Brainlab, the following specifications must be entered in RayPhysics. Everything in the MLC tab refers to the add-on MLC only. If the machine does not have jaws in the direction parallel to the MLC movement, the ordinary MLC may be used as a backup jaw to the add-on MLC. In this case, the Noback up jaw checkbox should not be checked, and the X1/X2 (in jaw labeling IEC 601: Y2/Y1) jaw constraints shall be specified according to the constraints for the ordinary MLC.*

If the machine has jaws in both x and y direction, the ordinary MLC shall be fixed to be fully retracted both during treatment and dose curve measurement. In this case, the ordinary MLC shall not be included when specifying the machine constraints in RayPhysics.

4.2.1 General properties

This section describes the **General** tab in the Machine constraints workspace.

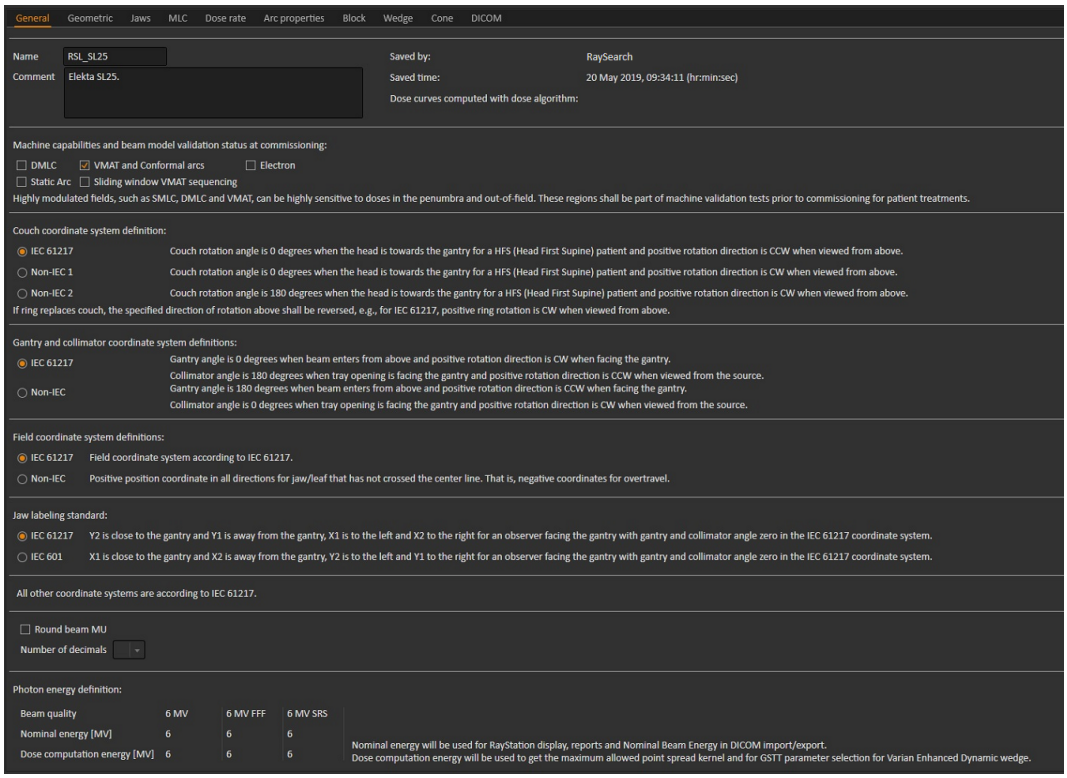

General
Geometric
Jaws
MLC
Dose rate
Arc properties
Block
Wedge
Cone
DICOM
Name
RSL_SL25
Comment
Elekta SL25.
Saved by:
RaySearch
Saved time:
20 May 2019, 09:34:11 (hr:min:sec)
Dose curves computed with dose algorithm:
Machine capabilities and beam model validation status at commissioning:
DMLC
VMAT and Conformal arcs
Electron
Static Arc
Sliding window VMAT sequencing
Highly modulated fields, such as SMLC, DMLC and VMAT, can be highly sensitive to doses in the penumbra and out-of-field. These regions shall be part of machine validation tests prior to commissioning for patient treatments.
Couch coordinate system definition:
IEC 61217
Couch rotation angle is 0 degrees when the head is towards the gantry for a HFS (Head First Supine) patient and positive rotation direction is CCW when viewed from above.
Non-IEC 1
Couch rotation angle is 0 degrees when the head is towards the gantry for a HFS (Head First Supine) patient and positive rotation direction is CW when viewed from above.
Non-IEC 2
Couch rotation angle is 180 degrees when the head is towards the gantry for a HFS (Head First Supine) patient and positive rotation direction is CW when viewed from above.
If ring replaces couch, the specified direction of rotation above shall be reversed, e.g., for IEC 61217, positive ring rotation is CW when viewed from above.
Gantry and collimator coordinate system definitions:
IEC 61217
Gantry angle is 0 degrees when beam enters from above and positive rotation direction is CW when facing the gantry.
Collimator angle is 180 degrees when tray opening is facing the gantry and positive rotation direction is CCW when viewed from the source.
Non-IEC
Gantry angle is 180 degrees when beam enters from above and positive rotation direction is CCW when facing the gantry.
Collimator angle is 0 degrees when tray opening is facing the gantry and positive rotation direction is CW when viewed from the source.
Field coordinate system definitions:
IEC 61217
Field coordinate system according to IEC 61217.
Non-IEC
Positive position coordinate in all directions for jaw/leaf that has not crossed the center line. That is, negative coordinates for overtravel.
Jaw labeling standard:
IEC 61217
Y2 is close to the gantry and Y1 is away from the gantry, X1 is to the left and X2 to the right for an observer facing the gantry with gantry and collimator angle zero in the IEC 61217 coordinate system.
IEC 601
X1 is close to the gantry and X2 is away from the gantry, Y2 is to the left and Y1 to the right for an observer facing the gantry with gantry and collimator angle zero in the IEC 61217 coordinate system.
All other coordinate systems are according to IEC 61217.
Round beam MU
Number of decimals
Photon energy definition:
Beam quality
6 MV
6 MV FFF
6 MV SRS
Nominal energy [MV]
6
6
6
Dose computation energy [MV]
6
6
6
Nominal energy will be used for RayStation display, reports and Nominal Beam Energy in DICOM import/export.
Dose computation energy will be used to get the maximum allowed point spread kernel and for GSTT parameter selection for Varian Enhanced Dynamic wedge.

Figure 49. The General tab in the Machine constraints workspace.

Name

This is the name of the LINAC which will be shown in RayStation and exported to DICOM. The name cannot be longer than 16 characters. The name of uncommissioned, template and commissioned machines must be unique.

Comment

This is a comment about the treatment machine visible to all users of the RayPhysics application.

Saved by / Saved time

These properties will be shown for uncommissioned machines the last time the machine was saved.

Dose curves computed with dose algorithm

These properties show the dose engine and dose engine version used to calculate the dose curves for uncommissioned machines.

- PhotonMonteCarlo = This is used for photon MC final dose computation.

- CCDose = This is used for photon CC final dose computation.
- ElectronMonteCarlo = This is used for electron MC final dose computation.

Commissioned by / Commission time

These properties will be shown for commissioned machines the last time the machine was commissioned.

Commissioned for dose algorithm

These properties show the dose engine and dose engine version used to calculate the dose curves for commissioned machines.

- PhotonMonteCarlo = This is used for photon MC final dose computation.
- CCDose = This is used for photon CC final dose computation.
- ElectronMonteCarlo = This is used for electron MC final dose computation.

Machine capabilities and beam model validation status

Here it is possible to define for which delivery techniques the beam commissioning is valid. This requires both that the machine and the R&V system have the capability to deliver this type of plans, and that the beam modeling and validation of the selected delivery technique has been performed successfully. In the RayPhysics Beam Commissioning module, the selection determines which machine properties are possible to edit. In RayStation, it determines which treatment and sequencing techniques that are available for the selected machine.

- **DMLC**: This property indicates that the machine model is usable for DMLC treatment. It is not possible to commission a machine with jaw movement rule **Fixed** for DMLC. The machine must also support MLC interdigitation. The DMLC plans created in RayStation are of "sliding window type" and for machines that have backup jaws, the jaws will not be moved when the beam is on.

  Depending on machine type, jaw movement rule and existence of backup jaws or not, different DMLC fluence calculation algorithms are used. For more information, refer to the *RSL-D-RS-9A-REF, RayStation 9A Reference Manual*.

- **Static arc**: This property indicates that the machine model is usable for rotational treatment using Static arcs, i.e., arcs where the MLC leaves and jaws are not allowed to move.
- **VMAT and Conformal arcs**: This property indicates that the machine model is usable for rotational treatment using the treatment techniques VMAT and Conformal arc.
- **Sliding window VMAT sequencing**: When VMAT plans are optimized in the Plan Optimization module in RayStation, the user can select sliding window leaf sequencing, where the leaves alternate between left-to-right and right-to-left unidirectional movement. Sliding window leaf sequencing is also used for VMAT plans created using the segment-based mode in the MCO module in RayStation.

This technique can be selected if the above option **VMAT and Conformal arcs** has been selected. Note that the machine must be set up for **Variable dose rate** and the MLC must support **Interdigitation**. Moreover, the **Use Arc burst mode** option cannot be selected.

- **Electron**: This property indicates that the machine model is usable for electron treatments. Certain machine parameters take on additional importance for electron capable machines. The jaw **Source to bottom distance** and **Thickness** will be used by the electron phase space engine, as will the **Source to MLC bottom distance** and **Thickness**.

The couch coordinate system

This selection determines the graphical user interface couch coordinate system in the main RayStation application and the RayPhysics 9A application. The following options are available:

- IEC 61217
- Non-IEC 1
- Non-IEC 2

Both IEC 61217 and Non-IEC 1 have couch rotation angle zero when the head is towards the gantry in the head first orientations. For the IEC 61217 the couch rotation angle increases counter-clockwise when looking from above. For the Non-IEC 1 the couch rotation angle increases clockwise looking from above.

For Non-IEC 2, the couch rotation angle is 180 degrees when the head is towards the gantry in the head first orientations. The couch rotation angle increases clockwise when viewed from above.

The coordinate system choice here influences both the main RayStation application and the RayPhysics 9A application.

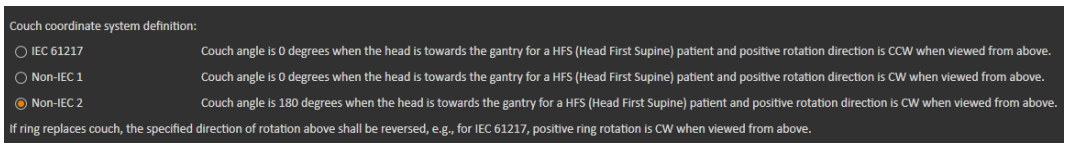

Couch coordinate system definition:
IEC 61217
Couch angle is 0 degrees when the head is towards the gantry for a HFS (Head First Supine) patient and positive rotation direction is CCW when viewed from above.
Non-IEC 1
Couch angle is 0 degrees when the head is towards the gantry for a HFS (Head First Supine) patient and positive rotation direction is CW when viewed from above.
Non-IEC 2
Couch angle is 180 degrees when the head is towards the gantry for a HFS (Head First Supine) patient and positive rotation direction is CW when viewed from above.
If ring replaces couch, the specified direction of rotation above shall be reversed, e.g., for IEC 61217, positive ring rotation is CW when viewed from above.

Figure 50. The couch coordinate system definition.

Pitch and roll always use IEC 61127

The pitch angle of the couch is zero when the patient is lying flat on the couch. Positive rotation direction is such that the head of an HFS (Head First Supine) patient is raised higher than the feet.

The roll angle of the couch is zero when the patient is lying flat on the couch. Positive rotation direction is such that the right side of an HFS (Head First Supine) patient is raised higher than the left side.

The gantry and collimator coordinate system

This selection determines the graphical user interface couch coordinate system in the main RayStation application and the RayPhysics 9A application. The following options are available:

- The **IEC 61217** gantry coordinate system has gantry angle zero when the beam enters from above and positive rotation direction clockwise when facing the gantry. The collimator coordinate system coincide with the gantry system when the collimator angle is zero. Positive rotation direction is counter clockwise when viewed from the source. For Varian machines, the collimator angle is usually 180 degrees when the tray opening is facing the gantry.
- The **Non-IEC** gantry coordinate system has gantry angle 180 degrees when beam enters from above and positive rotation direction counter clockwise when facing the gantry. The collimator coordinate system is rotated 180 degrees compared to the IEC 61217 coordinate system and positive rotation direction is clockwise when viewed from the source. For Varian machines, the collimator angle is usually zero degrees when the tray opening is facing the gantry.

The coordinate system choice here influences both the main RayStation application and the RayPhysics 9A application.

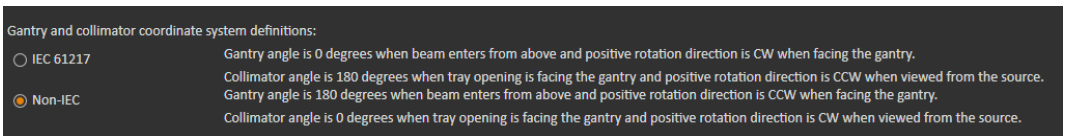

Gantry and collimator coordinate system definitions:
IEC 61217
Gantry angle is 0 degrees when beam enters from above and positive rotation direction is CW when facing the gantry.
Collimator angle is 180 degrees when tray opening is facing the gantry and positive rotation direction is CCW when viewed from the source.
Non-IEC
Gantry angle is 180 degrees when beam enters from above and positive rotation direction is CCW when facing the gantry.
Collimator angle is 0 degrees when tray opening is facing the gantry and positive rotation direction is CW when viewed from the source.

Figure 51. The gantry and collimator coordinate system definition.

The field coordinate system

This selection determines the graphical user interface field coordinate system in the main RayStation application and in the RayPhysics 9A application. The options are IEC 61217 and Non-IEC. For IEC, the collimator positions for a beam with (IEC) collimator angle 0 when viewed from the source are described in *The Field coordinate system definitions setting on page 35*.

For Non-IEC, positive position coordinates are reported in all directions for jaws and leaves that have not crossed the center line. That is, negative coordinates are reported for overtravel.

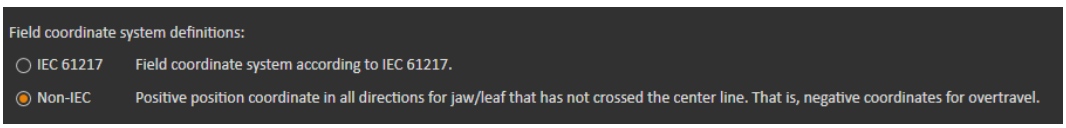

Field coordinate system definitions:
IEC 61217
Field coordinate system according to IEC 61217.
Non-IEC
Positive position coordinate in all directions for jaw/leaf that has not crossed the center line. That is, negative coordinates for overtravel.

Figure 52. The field coordinate system definition.

The jaw labeling standard

This selection determines the graphical user interface jaw labeling in the main RayStation application and in the Machine properties tabs in the RayPhysics application. In the beam model parameter workspace, the dose curve coordinate system is always used regardless of the selected jaw labeling standard. See *section 2.3.8 Dose curve coordinate system in RayPhysics on page 43* for more information. The following options are available:

- **IEC 61217**: Y2 is close to the gantry and Y1 is away from the gantry, X1 is to the left and X2 to the right for an observer facing the gantry with gantry and collimator angle zero in the IEC 61217 coordinate system.

- **IEC 601**: X1 is close to the gantry and X2 is away from the gantry, Y2 is to the left and Y1 to the right for an observer facing the gantry with gantry and collimator angle zero in the IEC 61217 coordinate system.

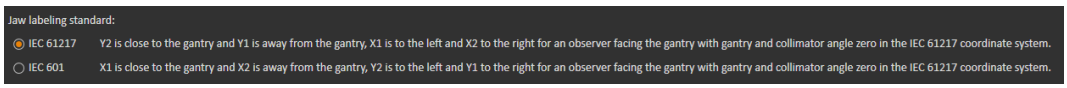

Jaw labeling standard:
IEC 61217
Y2 is close to the gantry and Y1 is away from the gantry, X1 is to the left and X2 to the right for an observer facing the gantry with gantry and collimator angle zero in the IEC 61217 coordinate system.
IEC 601
X1 is close to the gantry and X2 is away from the gantry, Y2 is to the left and Y1 to the right for an observer facing the gantry with gantry and collimator angle zero in the IEC 61217 coordinate system.

Figure 53. The jaw labeling standard definition.

Round beam MU

If the **Round beam MU** checkbox is checked, it is possible to select how many decimals (0, 1 or 2) the beam MU shall be rounded to.

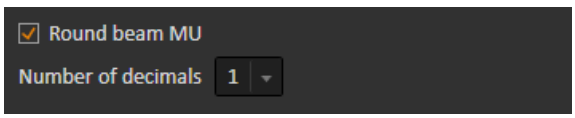


Figure 54. Round beam MU selected, and Number of decimals set to 1.

Photon energy definition

The dose computation energy and nominal energy are presented for all photon beam qualities. The **Nominal energy**, together with the **Fluence mode**, is used to label a beam quality in RayPhysics and RayStation. The **Dose computation energy** is used in dose computation and determines the photon energy spectrum. The energies cannot be changed here as they are set when a new photon beam quality is added.

For more information, see *section 3.4.1 Add photon beam quality on page 61*.

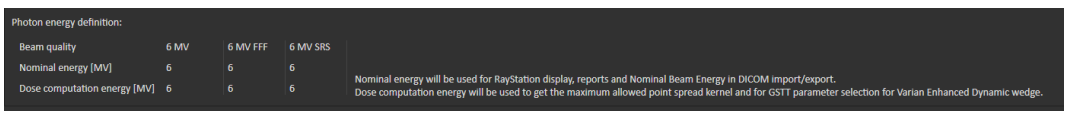

Photon energy definition:
Beam quality
6 MV
6 MV FFF
6 MV SRS
Nominal energy [MV]
6
6
6
Dose computation energy [MV]
6
6
6
Nominal energy will be used for RayStation display, reports and Nominal Beam Energy in DICOM import/export.
Dose computation energy will be used to get the maximum allowed point spread kernel and for GSTT parameter selection for Varian Enhanced Dynamic wedge.

Figure 55. The Photon energy definition.

4.2.2 Geometric properties

This section describes the **Geometric** tab in the Machine constraints workspace.

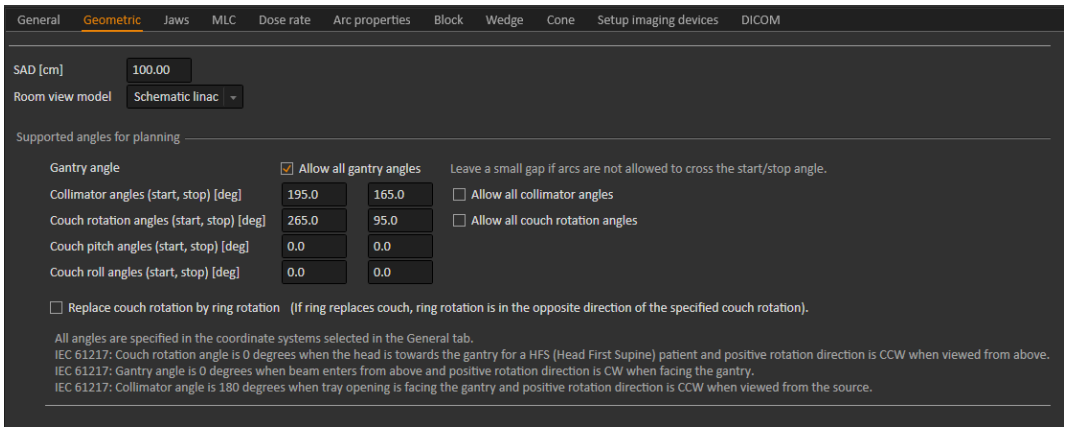

General
Geometric
Jaws
MLC
Dose rate
Arc properties
Block
Wedge
Cone
Setup imaging devices
DICOM
SAD [cm]
100.00
Room view model
Schematic linac
Supported angles for planning
Gantry angle
Allow all gantry angles
Leave a small gap if arcs are not allowed to cross the start/stop angle.
Collimator angles (start, stop) [deg]
195.0
165.0
Allow all collimator angles
Couch rotation angles (start, stop) [deg]
265.0
95.0
Allow all couch rotation angles
Couch pitch angles (start, stop) [deg]
0.0
0.0
Couch roll angles (start, stop) [deg]
0.0
0.0
Replace couch rotation by ring rotation
(If ring replaces couch, ring rotation is in the opposite direction of the specified couch rotation).
All angles are specified in the coordinate systems selected in the General tab.
IEC 61217: Couch rotation angle is 0 degrees when the head is towards the gantry for a HFS (Head First Supine) patient and positive rotation direction is CCW when viewed from above.
IEC 61217: Gantry angle is 0 degrees when beam enters from above and positive rotation direction is CW when facing the gantry.
IEC 61217: Collimator angle is 180 degrees when tray opening is facing the gantry and positive rotation direction is CCW when viewed from the source.

Figure 56. The **Geometric** tab.

The angles are specified in the coordinate systems defined in the **General** tab, including rotation direction, i.e. the supported angle interval increases from start angle to stop angle according to the rotation direction of the selected coordinate system. See *section 4.2.1 General properties on page 112* for more information.

SAD [cm]

The source axis distance (SAD) should be entered in cm.

Room view model

This selection decides how the machine is visualized in the Room View. The alternatives are: "Only couch", "Ring gantry" or "Schematic linac".

Supported gantry angles (start, stop) [deg]

This property sets the allowed angles for radiation treatment. Angles must be in the interval 0 to 360. Only one angular interval can be set up. Allowed angles range from start to stop towards increasing angles. If the start angle is larger than the stop angle the interval from start to 360 and from 0 to stop is allowed. For start 181 and stop 179 this gives an allowed gantry angle interval between 181 to 360 and 0 to 179. If all angles are allowed, check the **Allow all gantry angles** checkbox.

Note: *If the Allow all gantry angles checkbox is checked, arcs are allowed to pass through 0 - if that is not desired add a small gap between the start and the stop angle.*

Supported collimator angles (start, stop) [deg]

This property sets the allowed collimator angles for radiation treatment. The logic works the same as for the gantry angles described above.

Supported couch rotation angles (start, stop) [deg]

This property sets the allowed couch rotation angles for radiation treatment. The logic works the same as the gantry angles described above.

Couch pitch angles (start, stop) [deg]

This property sets the allowed couch pitch angles for radiation treatment. The logic works the same as the gantry angles above.

Couch roll angles (start, stop) [deg]

This property sets the allowed couch roll angles for radiation treatment. The logic works the same as the gantry angles above.

Replace couch rotation by ring rotation

If the **Replace couch rotation by ring rotation** checkbox is checked, then "Ring angle" will be displayed instead of "Couch angle" in the user interface. This would be the choice if a BrainLab Vero machine is used.

Beam line objects

If the machine can deliver electron fields, the following properties will be available in the **Geometric** tab:

- **Primary scattering foil z position**: The position of the first scattering foil the electron beam hits. This value is currently only used to calculate a starting guess for the Effective distance to source parameter in the electron beam model(s). It should be set to 0.
- **Secondary scattering foil z position**: The position of the secondary scattering foil the electron beam hits. The secondary scattering foil position determines where the simulation of the electron trajectories through the treatment head begins.
- **The machine has millstone**: If the machine has a millstone collimator, check this checkbox.

If the machine has a millstone, then the following properties are available:

- **Source to bottom distance** – the distance from the source to the lower edge of the millstone
- **Thickness** – the thickness
- **Inner opening X position** – dimension of the rectangular opening in X
- **Inner opening Y position** – dimension of the rectangular opening in Y
- **Focal point** - the z coordinate of the focal point which determines the angle of the millstone opening

4.2.3 Jaw properties

The jaw coordinate system and name convention are according to the selected values in the **General** tab. See *section 4.2.1 General properties on page 112* for more information. The selected coordinate system and name convention are specified at the bottom of the workspace.

General
Geometric
Jaws
MLC
Dose rate
Arc properties
Block
Wedge
Cone
DICOM
No backup jaw
Minimum Y2 jaw position [cm]
0.00
Maximum Y2 jaw position [cm]
20.00
Minimum X2 jaw position [cm]
-12.50
Maximum X2 jaw position [cm]
20.00
Jaw movement rule
Per segment
Reference field size X1/X2 [cm]
10.000
Reference field size Y1/Y2 [cm]
10.000
Maximum jaw speed [cm/s]
1.00
Jaw name convention is IEC 61217. Y2 is close to the gantry and Y1 is away from the gantry, X1 is to the left and X2 to the right for an observer facing the gantry with gantry and collimator angle zero in the IEC 61217 coordinate system.
Positive values are open positions, zero is aligned with isocenter and negative values overtravel the central position. The minimum position should be a numerically lower value than the maximum position for non-fixed jaws. The limits for the opposite jaw are assumed to be reflection symmetric.

Figure 57. The **Jaws** tab.

Source to Y1/Y2 (in jaw labeling IEC 601: X2/X1) jaw bottom distance [cm]

The distance from the source to the bottom of the Y1/Y2 (X2/X1) jaw. This option is only applicable when **No backup jaw** or **Electron beam capable** has been selected. For photon beam qualities this will be used to calculate field measure for machines without backup jaw. See *RSL-D-RS-9A-REF, RayStation 9A Reference Manual* for more information about the field measure calculation and the electron dose calculation.

Thickness Y1/Y2 (in jaw labeling IEC 601: X2/X1) jaw [cm]

The physical thickness of the Y1/Y2 (X2/X1) jaw. The thickness option is only applicable when **No backup jaw** or **Electron beam capable** has been selected. For photon beam qualities this will be used to calculate field measure for machines without backup jaw. See *RSL-D-RS-9A-REF, RayStation 9A Reference Manual* for more information about the field measure calculation and the electron dose calculation.

No backup Jaw

If the LINAC does not have jaws in the MLC direction (x direction in IEC61217 beam limiting device coordinate system), this box should be checked. This is the case for Siemens machines and Elekta machines with an Agility head.

Note: *Selecting "no backup jaw" enables the choice of Siemens Virtual Wedge and disables the choice of Varian Enhanced Dynamic Wedge. This means that for a machine which has a Varian Enhanced Dynamic Wedge, selecting "no back up jaw" will induce a deletion of the wedged curves, the wedge model and the wedge settings.*

Minimum Y2 (in jaw labeling IEC 601: X1) jaw position [cm]

The minimum position of the Y2 (X1) jaw is the position of the jaw where it over-travels the axis the most, or is closest to the central axis if over-travel is not allowed. This value is also applicable with opposite sign to the Y1 (X2) jaw position; -5 cm means that the jaw (both Y1 (X2) and Y2 (X1)) can move 5 cm past the central axis. The minimum Y2 (X1) jaw position is given on the isocenter plane.

Maximum Y2 (in jaw labeling IEC 601: X1) jaw position [cm]

The maximum position of the Y2 (X1) jaw is the most open position of the jaw. This value is also applicable with opposite sign to the Y1 (X2) jaw position; 20 cm means that the jaw (both Y1 (X2) and Y2 (X1)) can move 20 cm out from the central axis. The maximum Y2 (X1) jaw position is given on the isocenter plane.

Note: *When modeling a machine with an add-on MLC with extension smaller than the maximum physical jaw position of the LINAC, the maximum Y2 (X1) jaw position should be specified so that the jaws are never placed outside of the maximum opening of the add-on MLC in order to prevent leakage outside of the MLC.*

Minimum X2 (in jaw labeling IEC 601: Y1) jaw position [cm]

The minimum position of the X2 (Y1) jaw is the position of the jaw where it over-travels the axis the most, or is closest to the central axis if over-travel is not allowed. This value is also applicable with opposite sign to the X1 (Y2) jaw position; -5 cm means that the jaw (both X1 (Y2) and X2 (Y1)) can move 5 cm past the central axis. The minimum X2 (Y1) jaw position is given on the isocenter plane.

Maximum X2 (in jaw labeling IEC 601: Y1) jaw position [cm]

The maximum position of the X2 (Y1) jaw is the most open position of the jaw. This value is also applicable with opposite sign to the X1 (Y2) jaw position; 20 cm means that the jaw (both X1 (Y2) and X2 (Y1)) can move 20 cm out from the central axis. The maximum X2 (Y1) jaw position is given on the isocenter plane.

Note: *When modeling a machine with an add-on MLC with extension smaller than the maximum physical jaw position of the LINAC, the maximum X2 (Y1) jaw position should be specified so that the jaws are never placed outside of the maximum opening of the add-on MLC in order to prevent leakage outside of the MLC.*

Jaw movement rule

The jaw movement rule describes how the position of the jaws can be changed between segments. Chose **Fixed** if the LINAC is not capable of moving the jaws. Choose **Per segment** if the LINAC changes the jaws between segments, and choose **Per beam** if the LINAC changes the jaws between beams.

Note that DMLC plans created in RayStation for machines that have backup jaw will not have jaws that move when the beam is on, regardless of selected jaw movement rule.

Y2 (in jaw labeling IEC 601: X1) jaw position [cm]

The Y2 (X1) jaw position option is only applicable for a fixed jaw machine. It is the position of the Y2 (X1) jaw collimator edge in cm for a fixed jaw machine. This value is also applicable with opposite sign to the Y1 (X2) jaw position; 20cm means that the jaw (both Y1 (X2) and Y2 (X1)) are positioned at 20 cm out from the central axis. The Y2 (X1) jaw position is given on the isocenter plane.

X2 (in jaw labeling IEC 601: Y1) jaw position [cm]

The X2 (Y1) jaw position option is only applicable for a fixed jaw machine. It is the position of the X2 (Y1) jaw collimator edge in cm for a fixed jaw machine. This value is also applicable with opposite sign to the X1 (Y2) jaw position; 20 cm means than the jaw (both X1 (Y2) and X2 (Y1)) are positioned at 20 cm out from the central axis. The X2 (Y1) jaw position is given on the isocenter plane.

Reference field size

The reference field size is the field size used for LINAC calibration in the beam commissioning. The reference field size X1/X2 (Y2/Y1 in jaw labeling IEC 601) and reference field size Y1/Y2 (X2/X1 i jaw labeling IEC 601) are available in RayPhysics. These can be set to any value between 9.0 and 11.0 cm, but the field size 10 cm x 10 cm is common for almost all LINACs. To commission a beam model a depth dose curve must be imported for the reference field size. The reference field size is given on the isocenter plane.

Maximum jaw speed

The maximum jaw speed is used as a limit for jaw movement. The maximum jaw speed is given on the isocenter plane.

Beam splitting strategy

For machines that have a carriage (typically Varian) wide fields may be split when an SMLC or a DMLC plan is created.

If **Create new beams** is selected, then a beam split will result in the creation of new beams. If **Use multiple carriage groups** is selected, then there will be two or three 'carriage groups' in a split beam where each group has its own jaw position.

4.2.4 MLC properties

The MLC leaf center positions are given as y-coordinates (x-coordinates if MLC type is set to Y) in the IEC 61217 beam limiting device coordinate system.

The leaf-tip position limits are given according to the jaw name convention (IEC 61217 or IEC601) selected in the **General** tab. See *section 4.2.1 General properties on page 112* for more information.

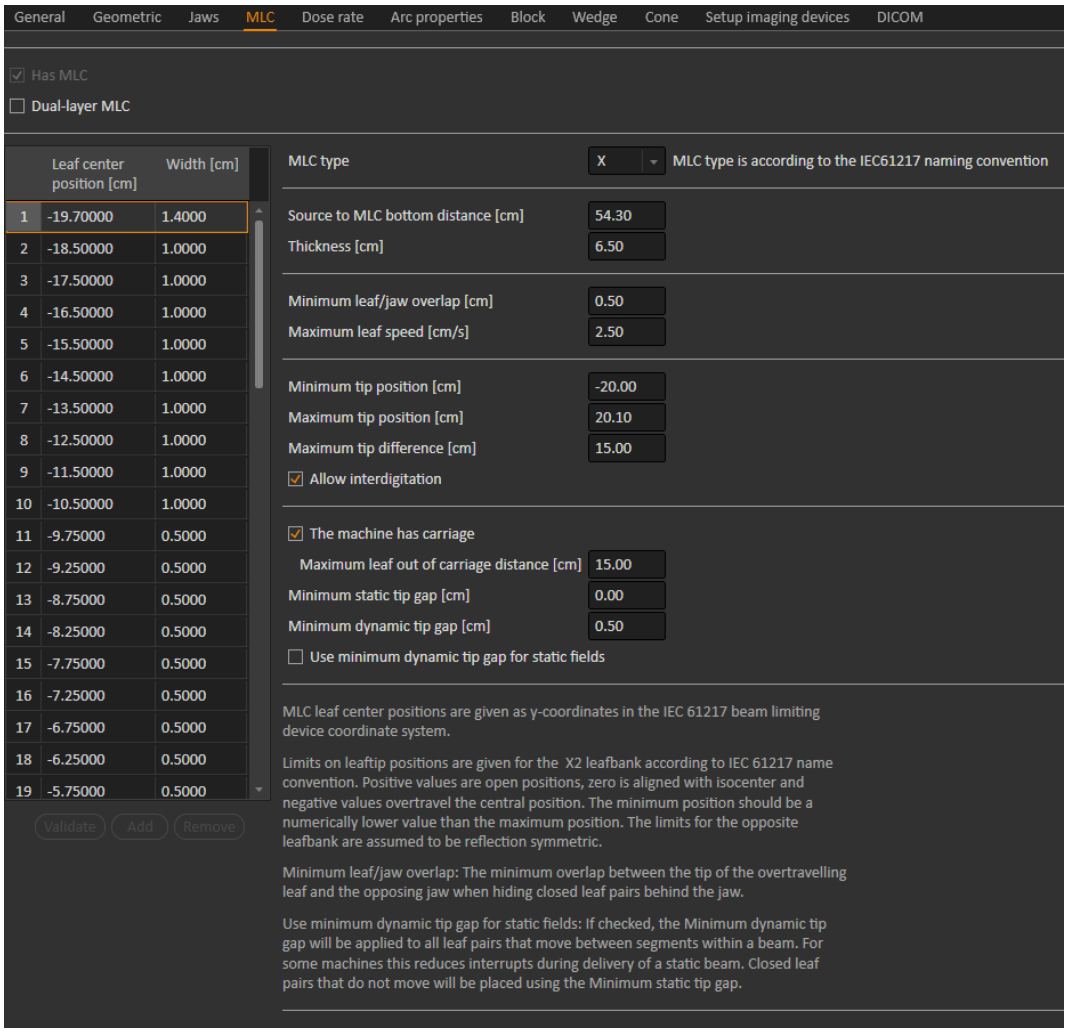

General
Geometric
Jaws
MLC
Dose rate
Arc properties
Block
Wedge
Cone
Setup imaging devices
DICOM
Has MLC
Dual-layer MLC
Leaf center position [cm]
Width [cm]
1 -19.70000 1.4000
2 -18.50000 1.0000
3 -17.50000 1.0000
4 -16.50000 1.0000
5 -15.50000 1.0000
6 -14.50000 1.0000
7 -13.50000 1.0000
8 -12.50000 1.0000
9 -11.50000 1.0000
10 -10.50000 1.0000
11 -9.75000 0.5000
12 -9.25000 0.5000
13 -8.75000 0.5000
14 -8.25000 0.5000
15 -7.75000 0.5000
16 -7.25000 0.5000
17 -6.75000 0.5000
18 -6.25000 0.5000
19 -5.75000 0.5000
Validate
Add
Remove
MLC type
X
MLC type is according to the IEC61217 naming convention
Source to MLC bottom distance [cm]
54.30
Thickness [cm]
6.50
Minimum leaf/jaw overlap [cm]
0.50
Maximum leaf speed [cm/s]
2.50
Minimum tip position [cm]
-20.00
Maximum tip position [cm]
20.10
Maximum tip difference [cm]
15.00
Allow interdigitation
The machine has carriage
Maximum leaf out of carriage distance [cm]
15.00
Minimum static tip gap [cm]
0.00
Minimum dynamic tip gap [cm]
0.50
Use minimum dynamic tip gap for static fields
MLC leaf center positions are given as y-coordinates in the IEC 61217 beam limiting device coordinate system.
Limits on leaftip positions are given for the X2 leafbank according to IEC 61217 name convention. Positive values are open positions, zero is aligned with isocenter and negative values overtravel the central position. The minimum position should be a numerically lower value than the maximum position. The limits for the opposite leafbank are assumed to be reflection symmetric.
Minimum leaf/jaw overlap: The minimum overlap between the tip of the overtravelling leaf and the opposing jaw when hiding closed leaf pairs behind the jaw.
Use minimum dynamic tip gap for static fields: If checked, the Minimum dynamic tip gap will be applied to all leaf pairs that move between segments within a beam. For some machines this reduces interrupts during delivery of a static beam. Closed leaf pairs that do not move will be placed using the Minimum static tip gap.

Figure 58. The **MLC** tab.

Has MLC

The **Has MLC** checkbox should be checked if the machine has MLC.

Dual-layer MLC

The **Dual-layer MLC** checkbox should be checked if the machine has two layers of MLC. Checking this checkbox will add a second MLC table with leaf center positions and widths.

Leaf center position and width

The MLC table to the left in the **MLC** tab lists the leaves and their position and width. The properties in this table are applied to both the left and right MLC leaves of an MLC leaf pair. The number of leaves entered should be the number of leaf pairs, which is half of the total number of leaves. The Leaf center position [cm] entry describes the center position of the leaves along the y-axis (x-axis if MLC type is set to Y) of the IEC61217 beam limiting device coordinate system. The Width [cm] entry describes the width of the individual MLC leaf in question, along the same axis as the center positions. The leaf center positions and widths are given on the isocenter plane. For machines with dual-layer MLC, there are two MLC tables, one for the Upper (proximal) layer and one for the Lower (distal) layer.

Note: *DICOM-export of leaf positions indicates the edge position of the leaf and not the central position, as in this table.*

Remove

MLC leaves marked in the table are deleted with the **Remove** button.

Add

Click the **Add** button to open a dialog to add new leaves to the table. In the Add leaves dialog the **Number of leaves** is the number of leaves to be generated. **Leaf center start position [cm]** defines the center position of the first leaf in cm. **Width [cm]** defines the width of a single leaf. Some LINACs have MLC with two different leaf widths. If this is the case, the different leaf regions must be added separately.

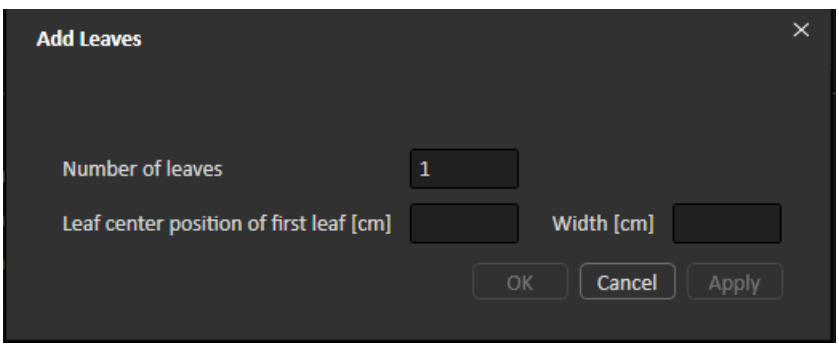


Figure 59. The **Add Leaves** dialog.

Validate

Validate that there are no overlaps or holes in the MLC-setup with this button.

MLC type

The movement direction of the MLC leaves. Can be X or Y. The X/Y direction is with regard to the IEC61217 beam limiting device coordinate system, regardless of the selected jaw labeling standard.

Note: *Machines with MLC movement direction Y are not supported together with cones, blocks, wedges or electrons.*

Source to MLC bottom distance [cm]

The distance from the source to the bottom of the MLC. This option is only applicable when **No backup jaw** or **Electron beam capable** has been selected. For photon beam qualities this will be used to calculate field measure for machines without backup jaw. See the *RSL-D-RS-9A-REF, RayStation 9A Reference Manual* for more information about the field measure calculation and the electron dose calculation.

Thickness [cm]

The physical thickness of the MLC. The thickness option is only applicable when **No backup jaw** or **Electron beam capable** has been selected. For photon beam qualities this will be used to calculate field measure for machines without backup jaw. See *RSL-D-RS-9A-REF, RayStation 9A Reference Manual* for more information about the field measure calculation and the electron dose calculation.

Minimum leaf jaw overlap [cm]

The minimum leaf jaw overlap determines the minimum overlap between the tip of the over-traveling MLC leaf and the opposing jaw when hiding closed leaf pairs behind the jaw. The minimum leaf jaw overlap is given on the isocenter plane.

Maximum leaf speed [cm/s]

The maximum leaf speed is used as a limit for leaf movement. The maximum leaf speed is given on the isocenter plane.

Note: *VMAT plans with large differences in MLC positions between consecutive control points may affect the dose computation time, since additional fluence computations are performed between control points. To limit the leaf travel, use the parameter Constrain leaf motion in the Settings dialog in the Plan Optimization module in RayStation. The accuracy of the dose computation may be improved by using Constrain leaf motion, and may be further improved by selecting a shorter gantry spacing.*

Minimum tip position [cm]

The minimum tip position is the position of the MLC where the leaf over-travels the axis the most, or is closest to the central axis if over-travel is not allowed; -5 cm means that the MLC-leaves (both left and right leaf bank) can move 5 cm past the central axis. The property is symmetric for the two leaf banks. The minimum tip position is given on the isocenter plane.

Maximum tip position [cm]

The maximum tip position is the most open allowed position of the MLC-leaves; 20 cm means that the MLC-leaves (both left and right) can move 20 cm out from the central axis. The property is symmetric for the two leaf banks. The maximum tip position is given on the isocenter plane.

Maximum tip difference [cm]

The maximum tip difference is the maximum possible distance between adjacent MLC leaf tips in the same MLC leaf bank. The maximum tip difference is given on the isocenter plane.

Allow interdigitation

The Allow interdigitation setting indicates that the machine is capable of letting opposite adjacent MLC leaves pass each other. For example if leaf number i in the left leaf bank is 4 cm away from the isocenter axis, leaf i+1 in the right left bank is still allowed to over-travel by more than 4 cm.

The machine has carriage

This box should be checked if the LINAC has a moving MLC-carriage from which the MLC-leaves are extended.

Note: *Questions related to carriage motion are important for beam splitting in SMLC and DMLC. Careful attention should be paid to these values.*

Maximum leaf out of carriage distance [cm]

The maximum distance that MLC leaves may travel out of the carriage. This property is disabled if the machine does not have a carriage. The maximum leaf out of carriage distance is given on the isocenter plane.

Minimum static tip gap [cm]

The minimum static tip gap is the minimum possible opening between opposite MLC leaves for static fields. The minimum static tip gap is given on the isocenter plane.

Minimum dynamic tip gap [cm]

The minimum dynamic tip gap is the minimum possible opening between opposite MLC leaves for dynamic fields such as VMAT beams. See *Use minimum dynamic gap for static fields on page 125* for more information. The minimum dynamic tip gap is given on the isocenter plane.

Use minimum dynamic gap for static fields

This property indicates that the machine requires the minimum dynamic tip gap to be fulfilled for leaf pairs that move between segments within a static beam. For some machines this reduces interruptions during delivery of a static beam.

4.2.5 Dose rate properties

In the **Dose rate** tab, dose rate settings for different treatment techniques are entered.

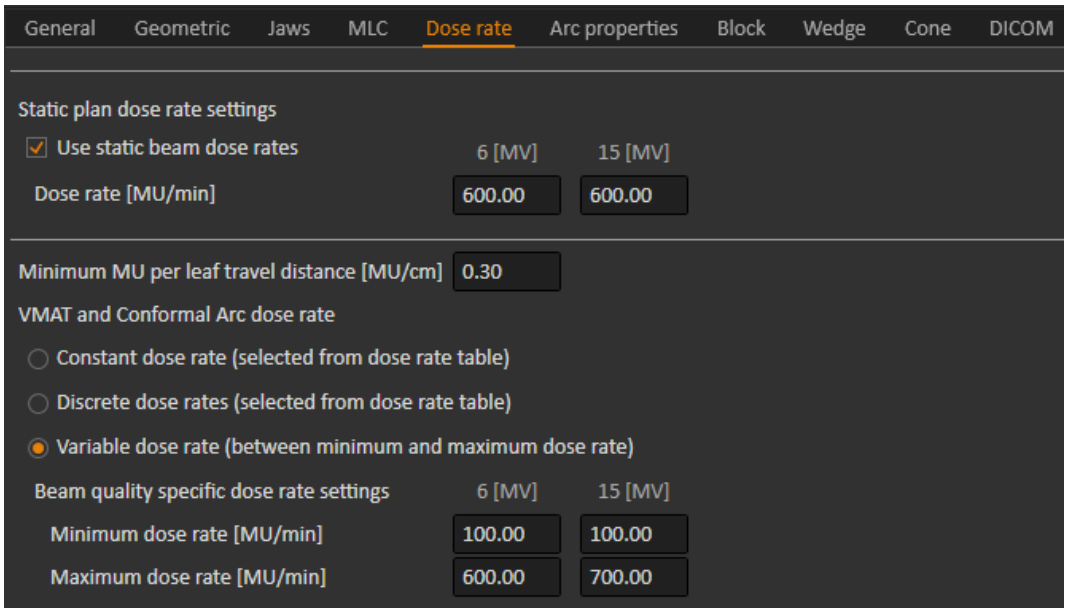


Figure 60. The **Dose rate** tab, where **Variable dose rate** has been selected.

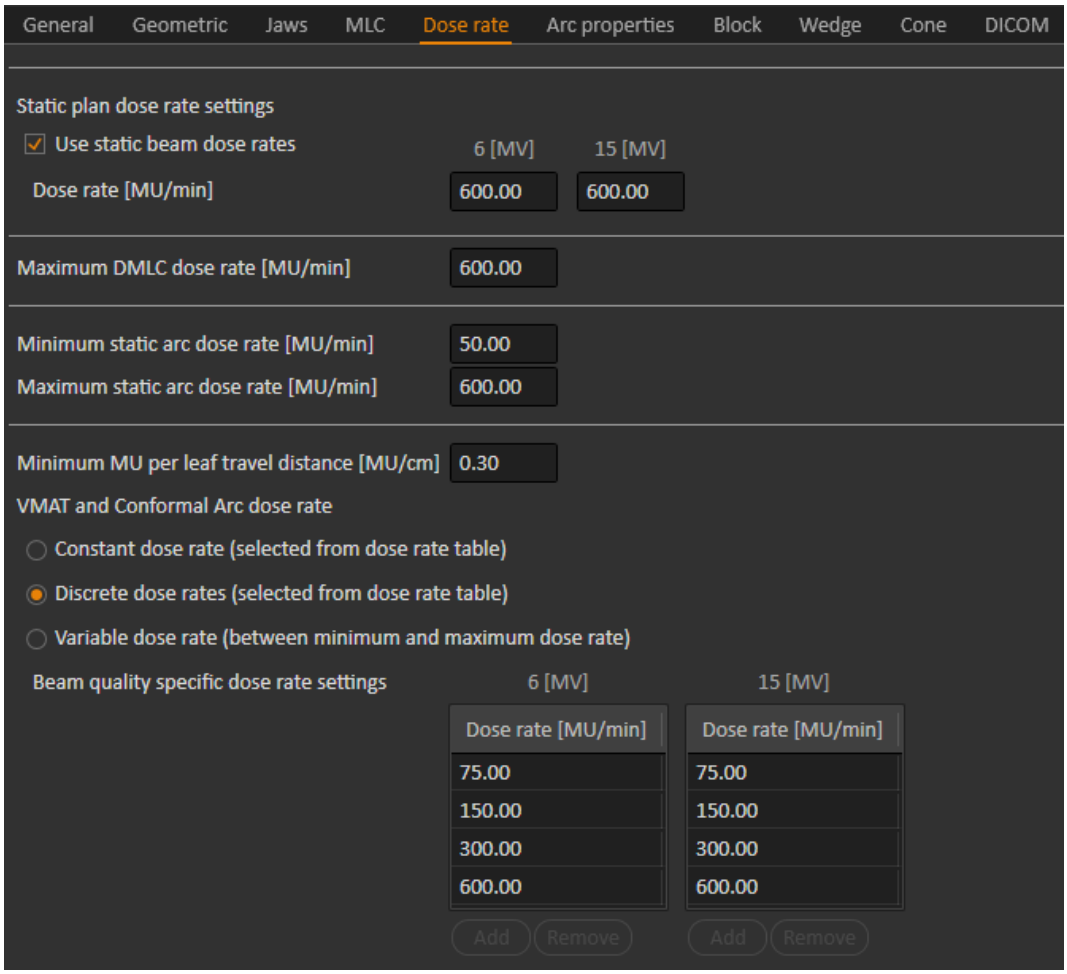


Figure 61. The **Dose rate** tab, where **Discrete dose rates** has been selected.

Static plan dose rate settings

Select to **Use static beam dose rates** by checking the corresponding checkbox.

Static plan dose rate [MU/min]

Dose rate used in DICOM export for static plans, i.e., 3D-CRT and SMLC plans. Must be specified for each beam quality (energy level). Only available if **Use static beam dose rates** is checked.

Maximum DMLC dose rate [MU/min]

The dose rate used in a DMLC plan that is created by optimization. Only applicable for DMLC capable machines.

Minimum and maximum Static arc dose rate [MU/min]

Allowed dose rate interval for a Static arc plan. Only applicable for Static arc capable machines.

Minimum MU per leaf travel distance [MU/cm]

For some machines there is a dependency between the minimum MU and the leaf travel distance. For these machines this property should be set. The minimum MU per leaf travel distance is used when optimizing and checking feasibility of VMAT and Conformal Arc plans. Only applicable for VMAT and Conformal Arc capable machines.

Dose rate type – constant, discrete or variable dose rate

Select whether the machine has a

- Constant dose rate (selected from a dose rate table)
- Discrete dose rates (selected from a dose rate table)
- Variable dose rate

A constant dose rate machine uses only one dose rate per arc selected from a list of discrete dose rates. A discrete dose rate machine can use several different dose rates per arc selected from a list of discrete dose rates. A variable dose rate machine varies dose rates continuously between a minimum and a maximum value.

Only applicable for VMAT and Conformal Arc capable machines.

Energy specific dose rate settings

Allowed dose rate values must be specified for each beam quality (energy level). Only applicable for VMAT and Conformal Arc capable machines.

Minimum dose rate [MU/min]

This is the minimum allowed dose rate for a variable dose rate machine. One value must be specified per beam quality. Only applicable for VMAT and Conformal Arc capable machines.

Maximum dose rate [MU/min]

This is the maximum allowed dose rate for a variable dose rate machine.One value must be specified per beam quality. Ensure that the maximum dose rate is larger than zero. If the maximum dose rate is zero it will not be possible to compute arc doses with the machine. Only applicable for VMAT and Conformal Arc capable machines.

Dose rate table [MU/min]

For machines with constant dose rate or discrete dose rates the allowed values are taken from a table with Dose rate [MU/min]. Add and remove values using **Add** and **Remove**. One table must be defined per beam quality. Only applicable for VMAT and Conformal Arc capable machines.

4.2.6 Arc properties

The **Arc properties** tab is only available for machines that are VMAT and Conformal Arc capable or Static arc capable.

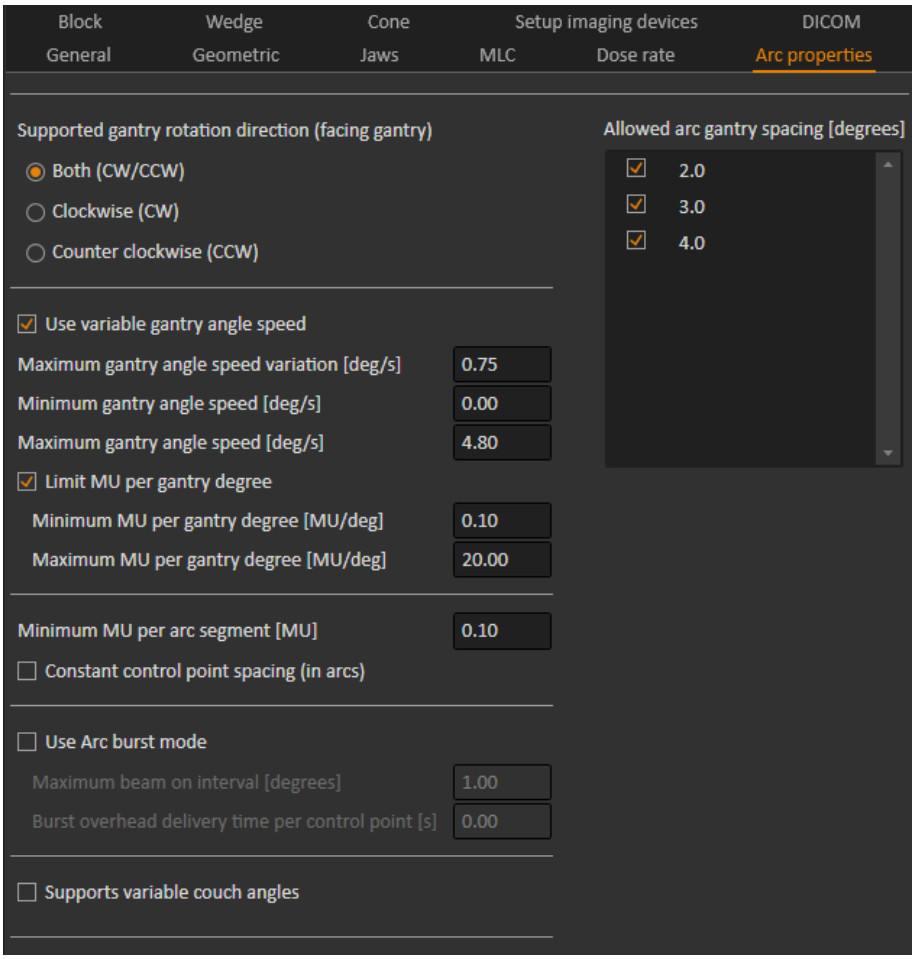


Figure 62. The **Arc properties** tab.

WARNING!

Modulated dynamic arc machines require information about collimator motion, gantry motion and dose rates. Deviation between the selected values and LINAC/R&V-system behavior may result in differences between delivered dose and dose approved in RayStation. (508981)

Supported gantry rotation direction

The supported gantry rotation directions can be both directions, clockwise or counterclockwise for an observer facing the gantry.

Allowed arc gantry spacing [deg]

When a VMAT optimization is performed the user selects the final arc spacing from a list of allowed values that are set up in beam commissioning.

The final arc spacing is the desired gantry angle spacing between two consecutive control points. This value together with the length of the arc determines the total number of control points of the arc. It also affects the dose accuracy, the computation time and the amount of modulation that can be achieved during optimization. Only applicable for VMAT and Conformal Arc capable machines.

Use variable gantry angle speed

This checkbox should be selected to obtain treatment plans with variable gantry angle speed. In this case the **Maximum gantry angle speed variation [deg/s]** shall be entered. Only applicable for VMAT and Conformal Arc capable machines.

VMAT plans created by using the default sequencing algorithm in RayStation (e.g., in the Plan Optimization module or by using the fluence-based mode in the Multi Criteria Optimization module) will use the maximum gantry angle speed or the maximum dose rate for each control point. VMAT plans created by using the sliding window leaf sequencing algorithm (e.g., in the Plan Optimization module or by using the segment-based mode in the Multi Criteria Optimization module) may create control points where both the dose rate and the gantry speed have values that are in-between the respective minimum and maximum allowed value.

Maximum gantry angle speed variation [degree/s]

This is the maximum allowed difference in gantry angle speed between two consecutive control points.

Minimum gantry angle speed [degree/s]

This is the minimum speed by which the gantry is allowed to rotate.

Maximum gantry angle speed [degree/s]

This is the maximum speed by which the gantry is allowed to rotate.

Limit MU per gantry degree

This checkbox should be selected if there is a restriction on how many MU that can be delivered per degree of gantry rotation. If the checkbox is selected the Minimum MU per gantry degree [MU/degree] and Maximum MU per gantry degree [MU/degree] shall be entered.

Minimum MU per gantry degree [MU/degree]

This is the minimum number of MU that can be delivered per degree of gantry rotation.

Maximum MU per gantry degree [MU/degree]

This is the maximum number of MU that can be delivered per degree of gantry rotation.

Minimum MU per arc segment [MU]

The minimum MU per arc segment is the lowest allowed MU that can be delivered between two consecutive control points. Only applicable for VMAT and Conformal Arc capable machines.

Constant control point spacing (in arcs)

If checked, the distance between consecutive control points of the wave arc must be constant in the dominant angle. For non-dynamic wave arcs, the dominant angle is the gantry angle. Note that in RayStation, dynamic wave arcs (described in *Supports variable couch angles on page 131*) are only supported with this option selected. Only applicable for VMAT and Conformal Arc capable machines.

Use Arc burst mode

This checkbox should be checked if the machine should use burst mode/mArc for treatment technique VMAT. This option is only available if variable dose rate is selected. If checked the beam is delivered using Burst technique, i.e., a rotating step and shoot beam. (Mainly used for arc capable Siemens machines.) Only applicable for VMAT and Conformal Arc capable machines. Machines commissioned to use burst mode cannot be used for Conformal Arc treatments.

Maximum beam on intervals [degrees]

Maximum beam on interval is the longest gantry rotation allowed when the beam is on for a Burst segment.

Burst overhead delivery time per control point [s]

The overhead time is used when estimating the delivery time for Burst beams. The time to deliver a control point in Burst mode is the time it takes to deliver the MU, plus the time it takes to move the leaves, plus a general overhead time (control system communication with the MLC). The overhead time is about one second for Siemens Artiste.

Supports variable couch angles

The **Supports variable couch angles** checkbox should be checked if the machine supports variable couch angles during the delivery of VMAT beams, i.e., if the machine is capable to deliver so called dynamic wave arcs. One machine that has this capability is the Brainlab Vero, for which the term ring angle is more appropriate than couch angle. However, in RayPhysics the term couch angle is used.

The parameters in the following table can only be entered for machines that support variable couch angles. Only applicable for VMAT and Conformal Arc capable machines.

Parameter	Description
Supported trajectory couch angles (start, stop) [deg]	This property sets the allowed couch angles for wave arcs. Angles must be in the interval 0 to 360. Only one angular interval can be set up. Allowed angles range from start to stop towards increasing angles. If the start angle is larger than the stop angle, intervals from start to 360 and from 0 to stop are allowed. The interval should be inside the supported couch angles for the machine.

Parameter	Description
Minimum couch angle speed [deg/s]	This is the minimum allowed couch angle speed for wave arcs.
Maximum couch angle speed [deg/s]	This is the maximum allowed couch angle speed for wave arcs.
Maximum trajectory slope	The largest trajectory slope that is acceptable when the non-dominant angle is viewed as a function of the dominant angle.
Same dominant angle for entire arc	This checkbox should be checked if the dominant angle is to be the same for the entire arc. Note that for individual sub-arcs the slope of the dominant angle as a function of the non-dominant angle may be larger than the slope of the non-dominant angle as a function of the dominant angle.

Dominant angle

The dominant angle is determined by computing:

i the largest slope of the couch angle as a function of the gantry angle, and

ii the largest slope of the gantry angle as a function of the couch angle.

If (i) < (ii), the gantry angle is the dominant angle. Otherwise, the couch angle that is the dominant angle. Should the couch angle be constant, the slope of the gantry angle as a function of the couch angle is considered to be infinite.

Example of trajectory for dynamic wave arc

Consider a trajectory with gantry angles = [340, 0, 40] and couch angles = [330, 0, 30]. The slope of the gantry angle as a function of the couch angle is then 20/30 and 40/30 for the two intervals (or sub-arcs), while the slope of the couch angle as a function of the gantry angle is 30/20 and 30/40 for the two intervals.

If the dominant angle is enforced to be the same for the entire arc, the couch angle is that dominant angle. To see this, note that the largest slope of the gantry angle as function of couch angle is 40/30, while the largest slope of the couch angle as function of the gantry angle is 30/20. Since 30/20 is larger than 40/30, the couch angle is dominant. It is then the value 40/30 that must not be larger than the maximum trajectory slope. On the other hand, if the dominant angle is not enforced to be the same throughout the arc, the couch angle is the dominant for the first interval, since 20/30 < 30/20, while the gantry angle is the dominant for the second interval since 30/40 < 40/30. In this case, neither 30/40 nor 20/30 must exceed the max trajectory slope.

4.2.7 Block properties

RayStation supports shielding blocks and aperture blocks, one of each type per beam. The distance from the primary source to the block tray and the block tray transmission is set in the Beam Commissioning module.

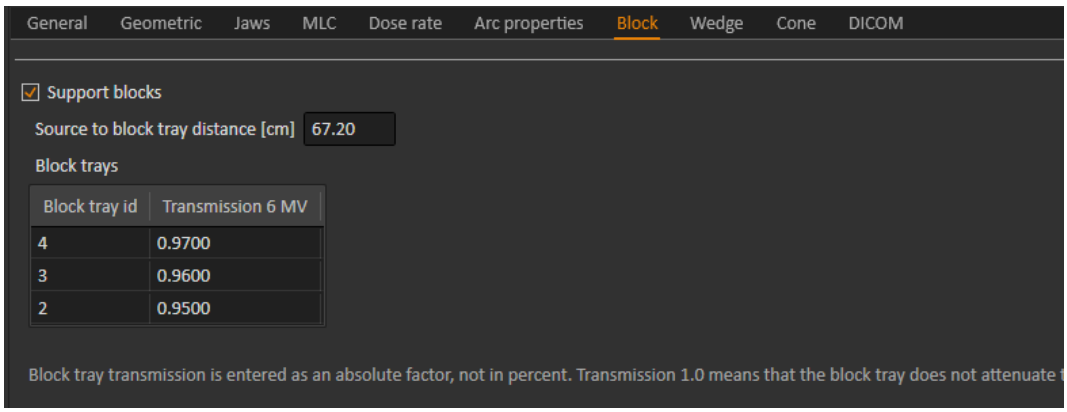


Figure 63. The **Block** tab.

WARNING!

Patient mistreatment. The dose engine assumes that blocks have zero thickness in the z-direction (perfect divergence). Always use blocks that are shaped for beam divergence.

Support blocks

If the LINAC supports blocks indicate this by checking **Support blocks** checkbox. Block transmissions are entered during planning.

Source to block tray distance [cm]

The **Source to block distance** value is used when projecting fluence through the block contour and in the DICOM export of plans with blocks.

Block trays

Enter **Block tray ID** and block tray transmission. The block tray transmission is entered as an absolute value, not in percent. Transmission 1.0 means that the block tray does not attenuate the beam at all. Several block trays may be added with transmission for one or several beam qualities. To commission a machine there must be at least one tray transmission entered for each beam quality supported by the machine.

4.2.8 Wedge properties

This section describes the **Wedge** tab in the Machine constraints workspace.

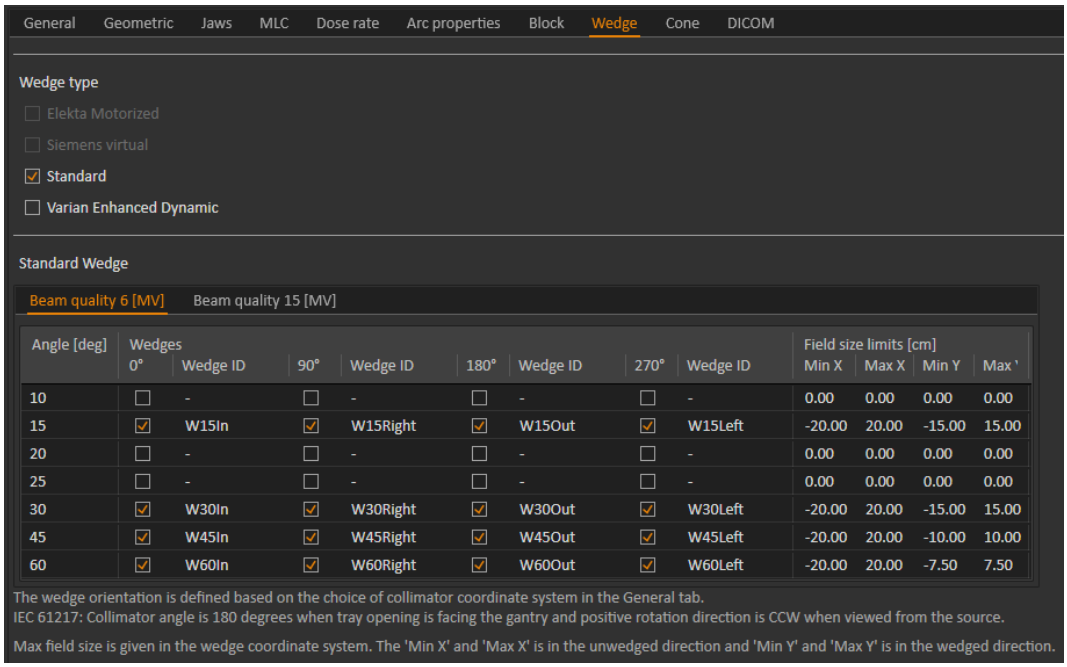

General
Geometric
Jaws
MLC
Dose rate
Arc properties
Block
Wedge
Cone
DICOM
Wedge type
Elekta Motorized
Siemens virtual
Standard
Varian Enhanced Dynamic
Standard Wedge
Beam quality 6 [MV]
Beam quality 15 [MV]
Angle [deg]
Wedges
0°
Wedge ID
90°
Wedge ID
180°
Wedge ID
270°
Wedge ID
Field size limits [cm]
Min X
Max X
Min Y
Max
10 - - - - - - 0.00 0.00 0.00 0.00
15 W15In W15Right W15Out W15Left -20.00 20.00 -15.00 15.00
20 - - - - - - 0.00 0.00 0.00 0.00
25 - - - - - - 0.00 0.00 0.00 0.00
30 W30In W30Right W30Out W30Left -20.00 20.00 -15.00 15.00
45 W45In W45Right W45Out W45Left -20.00 20.00 -10.00 10.00
60 W60In W60Right W60Out W60Left -20.00 20.00 -7.50 7.50
The wedge orientation is defined based on the choice of collimator coordinate system in the General tab.
IEC 61217: Collimator angle is 180 degrees when tray opening is facing the gantry and positive rotation direction is CCW when viewed from the source.
Max field size is given in the wedge coordinate system. The 'Min X' and 'Max X' is in the unwedged direction and 'Min Y' and 'Max Y' is in the wedged direction.

Figure 64. The **Wedge** tab.

Wedge type

There are four wedge types in RayPhysics 9A:

- Siemens Virtual
- Varian Enhanced Dynamic
- Elekta Motorized
- Standard

A machine that has **No backup jaw** selected (*No backup Jaw on page 120*) can support Siemens Virtual, Elekta Motorized or Standard wedges. A machine which does not have No backup jaw selected can support Varian Enhanced Dynamic, Elekta Motorized or Standard wedges.

A LINAC can support more than one wedge type, it is possible to select a Standard wedge and a Siemens Virtual wedge or a Varian Enhanced Dynamic wedge.

Allowed wedges

The list of allowed wedges is entered per beam quality. Any wedge angle and orientation combination can be selected or deselected individually. There is also the option to select all; this is reached by right-clicking in the wedge table.

Enabling wedge angles and orientations sets up the machine for import of corresponding wedged dose curves and is part of the set up for planning with wedges. Disabling wedge angles and orientations deletes the corresponding dose curves and model parameters.

The wedge orientation is defined relative to the selected collimator coordinate system. For IEC61217, the wedge orientation is zero degrees when the toe points towards the gantry for collimator angle zero and the wedge orientation angle increases with counter clockwise rotation of the wedge with respect to the beam limiting device system. This is further described in *section 2.3.4 The wedge filter coordinate system on page 38*.

- For Siemens Virtual Wedge the possible wedge angles are 15, 30, 45 and 60 degrees, both with orientation 0 degrees or 180 degrees.
- For Varian Enhanced Dynamic Wedge the allowed wedge angles are 10, 15, 20, 25, 30, 45 and 60, both with orientation 0 degrees or 180 degrees.
- For Elekta Motorized Wedge angles continuously up to 60 degrees can be used in RayStation but only 60 degrees can be selected in the Beam Commissioning module. Note that 60 degrees must be allowed for any other angle to be allowed. The only allowed orientation is 0 degrees (in non-IEC: 180 degrees).
- For standard wedges the possible wedge angles are 10, 15, 20, 25, 30, 45 and 60 degrees and the orientations are 0, 90, 180 and 270 degrees.

Note: *To import wedged curves, the wedge angle and orientation of the curves must be allowed. Only one orientation can be imported per wedge angle, but as long as curves for one orientation has been imported, all allowed orientations can be used in RayStation.*

Note: *If two different wedge types, e.g., standard and virtual, with the same angle are allowed, the user is asked to to choose which type a measurement describes when a dose curve is imported.*

Wedge-ID

The wedge-ID is used to communicate the wedge identity to the R&V-system using the DICOM interface. Each wedge angle and orientation combination must have a unique wedge-ID. For Siemens Virtual wedge the wedge-IDs are fixed. For Elekta Motorized and Standard wedges default wedge-IDs are automatically generated, but can be edited by the user.

Note: *The automatically generated wedge IDs may not correspond to the wedge naming at your clinic. Ensure that the wedge-ID is interpreted as intended by your R&V-system.*

Note: *When DICOM importing plans with wedges to RayStation, the matching of the wedge ID is case sensitive. For example, wedge ID EDW45IN will not be matched to EDW45In.*

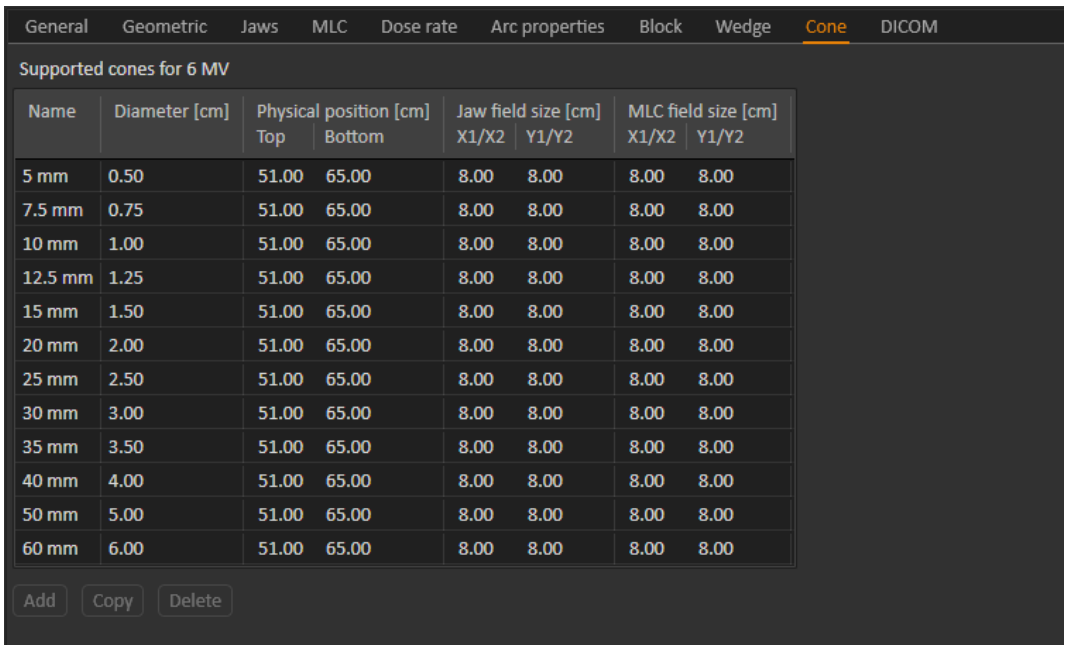
Maximum allowed wedged field size

The maximum allowed wedged field size must be specified for each selected wedge angle. The maximum field size is specified as a minimum and maximum coordinate in the X and Y directions. The X and Y directions are specified in the wedge coordinate system (see *section 2.3.4 The wedge filter coordinate system on page 38*), i.e., the X direction is in the direction perpendicular to the wedge and the Y direction is in the wedged direction. The maximum field size is given on the isocenter plane.

Note: *Make sure that you have measured curves up to the maximum allowed field size in order to evaluate your beam fit. This is especially important for physical wedges.*

4.2.9 Cone properties

In the **Cone** tab in the Machine constraints workspace, it is possible to specify that the machine supports circular cones. Circular cones are a type of aperture block with a small, fixed circular opening that is attached directly to the machine without a tray.



Name	Diameter [cm]	Physical position [cm] Top	Physical position [cm] Bottom	Jaw field size [cm] X1/X2	Jaw field size [cm] Y1/Y2	MLC field size [cm] X1/X2	MLC field size [cm] Y1/Y2
5 mm	0.50	51.00	65.00	8.00	8.00	8.00	8.00
7.5 mm	0.75	51.00	65.00	8.00	8.00	8.00	8.00
10 mm	1.00	51.00	65.00	8.00	8.00	8.00	8.00
12.5 mm	1.25	51.00	65.00	8.00	8.00	8.00	8.00
15 mm	1.50	51.00	65.00	8.00	8.00	8.00	8.00
20 mm	2.00	51.00	65.00	8.00	8.00	8.00	8.00
25 mm	2.50	51.00	65.00	8.00	8.00	8.00	8.00
30 mm	3.00	51.00	65.00	8.00	8.00	8.00	8.00
35 mm	3.50	51.00	65.00	8.00	8.00	8.00	8.00
40 mm	4.00	51.00	65.00	8.00	8.00	8.00	8.00
50 mm	5.00	51.00	65.00	8.00	8.00	8.00	8.00
60 mm	6.00	51.00	65.00	8.00	8.00	8.00	8.00

Figure 65. The **Cone** tab.

Cones are added per beam quality, and for each cone the following properties are specified:

- **Name** – name of the cone that will be visualized in RayStation and written as Applicator ID in the DICOM export. The cone name must be unique within a beam quality.
- **Diameter** – diameter of the circular opening of the cone. The cone diameter must be unique within a beam quality. The cone diameter is given on the isocenter plane.
- **Physical position, Top** – distance from the top of the cone to the source.
- **Physics position, Bottom** – distance from the bottom of the cone to the source.
- **Jaw field size**, X1/X2 (in jaw labeling IEC 601: Y2/Y1) – the jaw field size that should be used when setting up a beam with this cone. The jaw field size is given on the isocenter plane.
- **Jaw field size**, Y1/Y2 (in jaw labeling IEC 601: X2/X1) – the jaw field size that should be used when setting up a beam with this cone. The jaw field size is given on the isocenter plane.
- **MLC field size**, X1/X2 (in jaw labeling IEC 601: Y2/Y1) – the MLC field size that should be used when setting up a beam with this cone. The MLC field size is given on the isocenter plane.

- **MLC field size**, Y1/Y2 (in jaw labeling IEC 601: X2/X1) – the MLC field size that should be used when setting up a beam with this cone. The field size must be possible to achieve with the specified MLC leaves of the machine. The MLC field size is given on the isocenter plane.

Clicking the **Add** button will add a new cone with default values. **Copy** will create a copy of the selected cone with a new default name and diameter. **Delete** will delete the selected cone.

4.2.10 DICOM

This section describes the **DICOM** tab in the Machine constraints workspace.

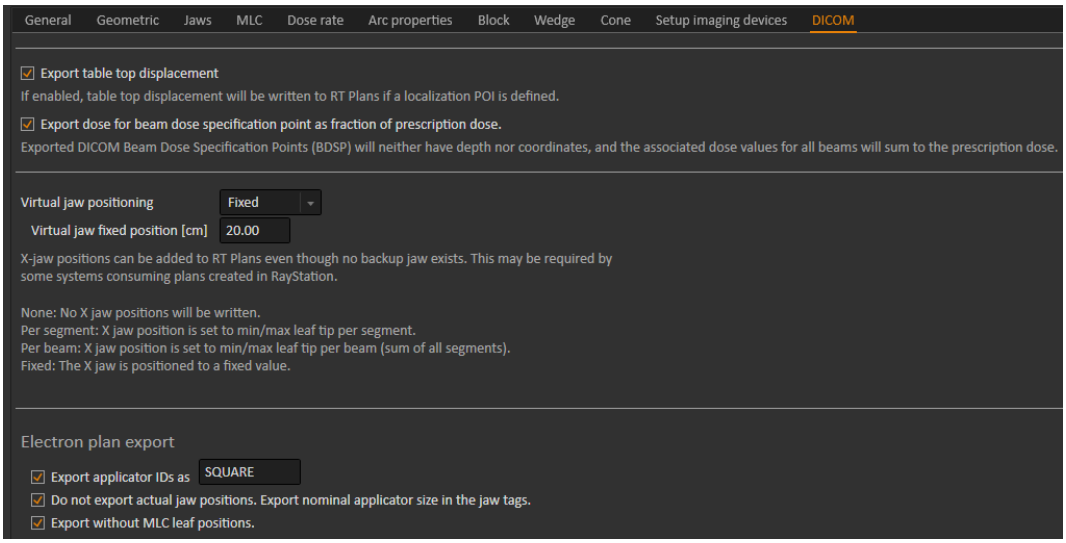

General
Geometric
Jaws
MLC
Dose rate
Arc properties
Block
Wedge
Cone
Setup imaging devices
DICOM
Export table top displacement
If enabled, table top displacement will be written to RT Plans if a localization POI is defined.
Export dose for beam dose specification point as fraction of prescription dose.
Exported DICOM Beam Dose Specification Points (BDSP) will neither have depth nor coordinates, and the associated dose values for all beams will sum to the prescription dose.
Virtual jaw positioning
Fixed
Virtual jaw fixed position [cm]
20.00
X-jaw positions can be added to RT Plans even though no backup jaw exists. This may be required by some systems consuming plans created in RayStation.
None: No X jaw positions will be written.
Per segment: X jaw position is set to min/max leaf tip per segment.
Per beam: X jaw position is set to min/max leaf tip per beam (sum of all segments).
Fixed: The X jaw is positioned to a fixed value.
Electron plan export
Export applicator IDs as
SQUARE
Do not export actual jaw positions. Export nominal applicator size in the jaw tags.
Export without MLC leaf positions.

Figure 66. The **DICOM** tab.

Export table top displacement

If the **Export table top displacement** checkbox is checked, the table top displacement will be written to RT Plans if a localization POI is defined.

Export dose for beam dose specification point as fraction of prescription dose

If the **Export dose for beam dose specification point as fraction of prescription dose** is checked, the BDSP dose will be exported as a fraction of the prescription (not according to DICOM standard). The sum of BDSP dose over all beams and fractions will equal the prescription dose. The BDSP dose will be distributed among the beams based on their beam MU. Since this dose value is not related to the BDSPs shown in RayStation, no coordinates or depths will be exported.

Virtual jaw positioning

The positions of the x-jaws can be added to RT Plans even though no backup jaw exists. This may be required by some systems consuming plans created in RayStation 9A. Only available for machines that have No backup jaw selected. The following options are available:

- **None**: No x jaw positions will be written.
- **Per segment**: x jaw position is set to min/max leaf tip per segment.
- **Per beam**: x jaw position is set to min/max leaf tip per beam (sum of all segments).
- **Fixed**: The x jaw is positioned to a fixed value.

If **Fixed** is selected, the position of the jaw is entered as **Virtual jaw fixed position**.

Electron plan export

The electron plan export options affect how electron RT Plans are exported from RayStation. These options may be needed to resolve interoperability problems.

Editing the electron settings will affect dosimetrically relevant attributes. The exported plan will not correspond to what was used for dose calculation in RayStation. DICOM round trip is not supported. Re-import of such plans will read the changed settings from the file, causing a stopped or adjusted dose computation.

- **Export applicator IDs as** - If this checkbox is checked, it is possible to override the Applicator IDs. The same ID will then be used throughout the RT Plan for all applicators.
- **Do not export actual jaw positions** - If this checkbox is checked, the nominal field size given for each applicator will be used to set symmetric jaw positions in the RT Plan.
- **Export without MLC leaf positions** - If this checkbox is checked, no MLC leaf position information will be exported.

4.3 BEAM MODEL PARAMETERS FOR PHOTONS

This chapter describes the beam model parameters. Each LINAC and beam quality has its own beam model which is used to compute dose.

In this section

This section contains the following sub-sections:

4.3.1	Fluence	p. 142
4.3.2	Energy spectrum	p. 146
4.3.3	Off axis	p. 148
4.3.4	Output factor corrections	p. 150
4.3.5	Physical wedges	p. 152
4.3.6	Siemens virtual wedge	p. 154
4.3.7	Varian enhanced dynamic wedges	p. 155
4.3.8	Wedge factor corrections	p. 156
4.3.9	Cone factor corrections	p. 157
4.3.10	Summary of the beam model parameters	p. 158

Precautions

WARNING!

Beam model quality depends on beam data. The quality of the beam model depends critically on the quality and scope of the beam data, for example, dose curves, output and wedge factors, absolute calibration, phantom size and collimation settings which influence the curve field setup. The entered measurement conditions must match the measurement technique. The sizes of the measured fields should cover the field sizes of the future applications of the beam model.

All input data, such as measured curves and output factors, must be coherent and correspond to the delivery system which is to be commissioned. Otherwise the generated beam model will not be able to calculate a correct dose.

For more information, refer to the *RSL-D-RS-9A-BCDS, RayStation 9A Beam Commissioning Data Specification*. (508979)

4.3.1 Fluence

The **Fluence** tab contains parameters used in the dose computation. For distances to source and transmissions one can either start by adding values that correspond to the specifications given by the hardware manufacturer or one can start from the corresponding template. When using a template please check that the values are in reasonable agreement with hardware manufacture specifications. The parameters can be viewed as effective computation parameters, where a good start guess can be taken from the machine template or machine specifications.

The distances to source, transmissions and additional MLC parameters are not part of auto-modeling scripts; they can be adjusted manually but they should not differ significantly from measured transmissions or known hardware specifications. Widths and weights can either be edited manually or adjusted using auto-modeling steps.

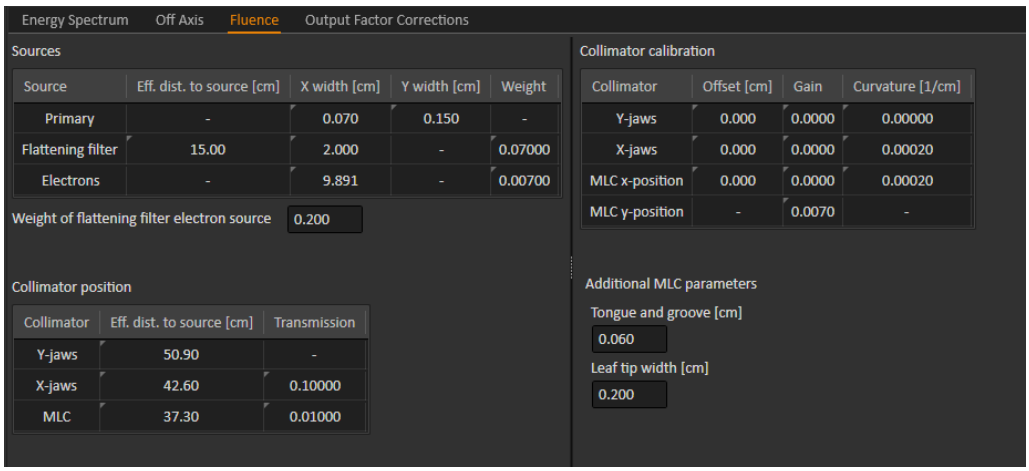


Figure 67. The Fluence tab.

Effective distance to source

The effective distance to source should be entered for the Flattening filter source and for all the Collimators (MLC, YJaws and when applicable XJaws). It is the effective distance between the primary photon source target and the collimator in question or the Flattening filter source expressed in cm. The target is defined to be located at the origin and the isocenter at +SAD cm. The sources and collimators are modeled to have no extension in the z direction; therefore there is no exact correspondence to the real hardware, but a good approximation is usually the distance from the bottom of each of the required items. The collimator effective distances are used for the source projection in the fluence computation part of the dose computation (refer to the *RSL-D-RS-9A-REF, RayStation 9A Reference Manual* for more information). For dual-layer MLC machines, the effective distance to source shall be entered for both the upper and the lower MLC layer. The position of the upper MLC layer is used in the fluence computation.

Transmission

The transmission should be entered for the XJaws (if the machine has backup jaws) and the MLC. The value to be entered shall be in absolute values (<1), not in percent. The YJaws are currently modeled to have zero transmission. For dual-layer MLC machines, it is possible to enter transmission for both the upper and the lower MLC layer. It is however required that both layers have the same transmission, which is checked upon commissioning of the machine.

For a machine with MLC type set to Y, transmission should instead be entered for the YJaws. The XJaws are modeled to have zero transmission.

For the MLC, interleaf leakage is not taken into account separately. This may be accounted for by increasing the value of the MLC transmission to get a correct average transmission.

Flattening filter weight

The flattening filter weight is the relative source strength of the flattening filter source compared to the source strength of the total photon contribution, i.e. two photon sources, primary and flattening filter. The sum is always 1.0 which is why the value entered must be less than one. Using the template machine values is the best starting point to use for modeling.

Electron source weight

The electrons source weight is the relative electron source strength compared to the source strength of the two photon sources. Electron energy fluence is not converted to dose in the same way as photon fluence which is why this source strength relation does not translate into dose from electron vs. dose from photons at some specific depth. Use the electron source weights to get the right buildup dose to match measured dose curves. Again, the template values are the best place to start. Auto-modeling will adjust these values as necessary to get a better fit.

Weight of flattening filter electron source

The electron fluence is sub-divided into fluence from a primary source positioned at the primary photon target and a secondary source positioned at the flattening filter target with the same width as the flattening filter. This weight is the relative fraction of the total electrons that will originate from the secondary electron source positioned at the flattening filter.

Source widths

The primary source can have different widths in x and y. Using that feature note that the source does not rotate with the collimator. The flattening filter and the electron sources have the same widths in x and in y.

The widths are the standard deviation of the source strength distribution indicated at the source z-position.

Tongue and groove [cm]

The tongue and groove region is a region centered at the leaf side, where the transmission is modeled to be the square root of the MLC transmission. The total tongue and groove region will be twice the size of the value entered for the tongue and groove parameter, since a region with the size of the tongue and groove parameter will be added to both sides of the leaf side. For dual-layer MLC machines, the same collimator calibration is used for both MLC layers.

The size is indicated as the size of the region when projected from the primary source onto the isocenter plane. The tongue and groove geometry information may be provided by the LINAC vendor. Start with a tongue and groove region which is approximately the same size as the geometric tongue and groove region projected onto the isocenter plane and tune the value to match measurement.

Leaf tip width [cm]

The leaf tip width is the width of a region from the leaf tip towards the leaf base, where the transmission is modeled to be the square root of the MLC transmission. For dual-layer MLC machines, the same leaf tip width is used for both MLC layers. The size is indicated as the size of the region when projected from the primary source onto the isocenter plane. The leaf tip geometry information may be provided by the LINAC vendor. Start with a leaf tip region which is approximately the same size as the geometric leaf tip region projected onto the isocenter plane and tune the value to match measurement.

Note: *MLC collimated square fields can be used to evaluate these parameters in the Beam Commissioning module. But for complete MLC modeling the user should also use 3D dose distributions captured with QA tools (for example film, EPID or other QA devices with sufficient resolution) for different test fields such as picket fence fields. These fields can be set up in the Beam 3D Modeling module and evaluated in external systems.*

Collimator calibration

Using flat collimators in fluence projections may necessitate position adjustments to get a perfect match for penumbra positions. The collimator calibration parameters can be used to achieve this by adjusting the effective collimator positions used in the dose computation. The XJaws and the MLC leaves are adjusted so that:

Left MLC bank:

$$x_{usedinprojections} = x_{nominal} - Offset + Gain \cdot x_{nominal} - Curvature \cdot x_{nominal}^2 \quad \text{[Eq. 2]}$$

Right MLC bank:

$$x_{usedinprojections} = x_{nominal} + Offset + Gain \cdot x_{nominal} + Curvature \cdot x_{nominal}^2 \quad \text{[Eq. 3]}$$

The nominal x in Equation 2 and Equation 3 is used in all visualizations, beam lists and DICOM import and export. It is expressed in IEC 61217 field coordinate system, i.e., will be negative when a leaf from either left or right MLC bank is on the left side of the origin. The same option is available for the YJaws in the y direction. The MLC leaves also have a gain term in y. As a rule of thumb put these values to zero and adjust only after having worked on source sizes, leaf tip widths and tongue and groove.

For a machine with MLC type set to Y, the opposite applies, i.e., there is offset, gain and curvature in y and only a gain term in x.

A positive offset enlarges all fields by this exact offset. Positive gain shifts the leaf position outwards by an increasing amount with the distance from the origin. The shift will be to the left if the leaf is to the left of the origin independent of the leaf bank, and vice versa for the right side. Positive curvature enlarges the fields by an increasing amount with the distance from the origin. A curvature of 0.01/cm gives a shift of 1 cm for an MLC position of 10 cm.

WARNING!

Collimator calibration. The collimator calibrations (offset, gain and curvature) are used to shift the collimator positions from the plan positions (shown in the Beam's Eye View, in beam lists, in reports, exported in DICOM etc.) to an effective position used in dose computation. For dose curves this only shifts the penumbra, but for a VMAT, SMLC or DMLC field with many segments adding up, this can change the overall dose level. Ensure that the collimator shift in the beam model is really intended. Be extra careful with gain and curvature shifts which increase with increasing distances from the origin. Results from the auto-modeling collimator calibration step must be reviewed before clinical use. (508988)

4.3.2 Energy spectrum

Photon energy spectrum

The photon energy spectrum on the central axis is entered as a list of mono-energetic contributions which combine to give a poly-energetic spectrum used in dose computation. All energy bins are smaller or equal to the dose computation energy of the machine model, i.e., with energy bins up to 6 MeV for a beam quality with dose computation energy 6 MV. The spectrum can be normalized such that the energy fluence is 1 MeV using Normalize Spectrum. This changes the overall normalization of the beam model which can be corrected for by changing the normalization in the output factor corrections tab. When auto-modeling the energy spectrum this normalization is automatically performed.

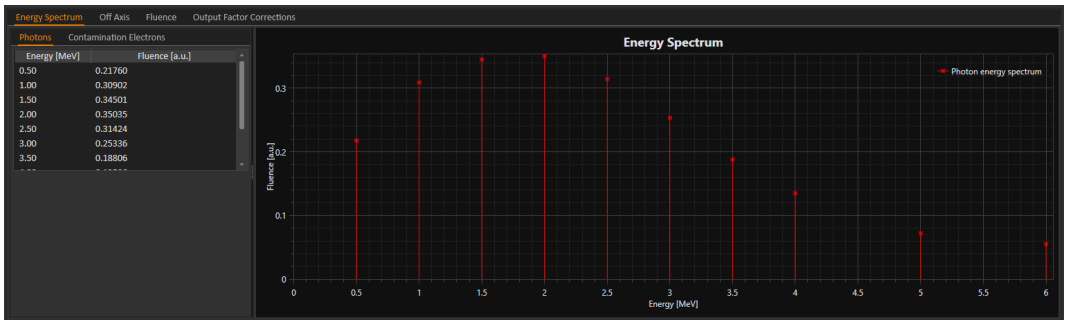


Figure 68. The Energy spectrum tab, where the Photons sub-tab has been selected.

To change the photon parameters select the energy to be adjusted from the Energy [MeV] list and enter the new fluence in a.u. in the next field. The spectrum will be normalized automatically if the **Normalize on Add** checkbox is checked. The spectrum can also be normalized manually once all the values are edited by clicking the **Normalize spectrum** button. When satisfied with the depth dose curves below D_{max}, turn to the electron parameters.

A spectrum bar in RayPhysics 9A specifies integrated particle fluence weights at the energy of the bar. When comparing to an analytical shape the weight is obtained by integrating over an energy range starting/ending halfway between the neighboring bars. For most points this results in symmetrical and equidistant intervals . At some energies there is a jump to a coarser grid resulting in a spectrum shape which looks unphysically skewed as the high energy bins are integrated over a larger energy interval. This is particularly visible when using the parameterized energy spectrum auto-modeling step.

Electron energy spectrum

The electron energy spectrum is described by two parameters, $\mathcal{E}_0$ and c.

$$f(E) \propto E^c e^{-E/E_0} \qquad \text{[Eq. 4]}$$

The parameter $\mathcal{E}_0$ determines the exponential fall-off, and c reduces the number of low-energy electrons. Typical values for 6 MV photon beams are $\mathcal{E}_0$ between zero and one MeV and c between zero and one. The electron energy fluence is normalized such that the area under the curve is 1 MeV.

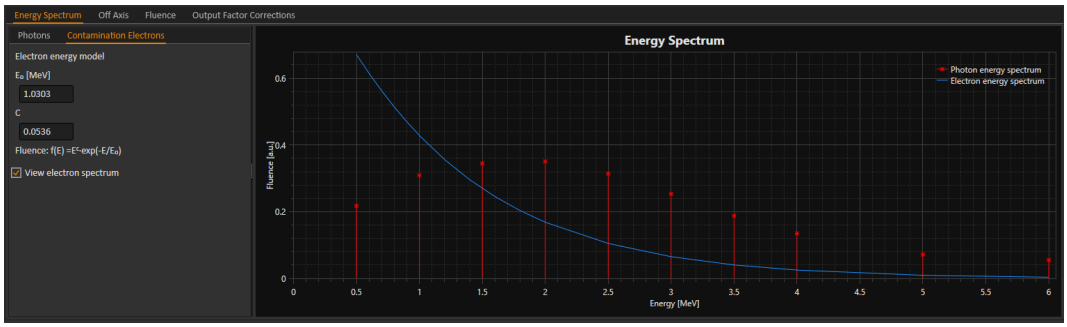


Figure 69. The Energy spectrum tab, where the Electrons sub-tab has been selected.

4.3.3 Off axis

Off-axis softening

The energy spectrum off-axis is related to the energy spectrum at radius zero (*Photon energy spectrum on page 146*) using the off-axis softening. The off-axis softening values are entered as negative water equivalent thicknesses off-axis.

Delete an entry by selecting it in the table and clicking **Delete**. Add a new entry by editing the boxes below the table and click **Add/Edit**. Change the Water equivalent thickness for the point at a given radii by marking the row in the table and editing the Water equivalent thickness in the box below the table, then click **Add/Edit**. Note that marking a row, changing the Radius and clicking Add/Edit creates a new entry and does not delete the originally selected value.

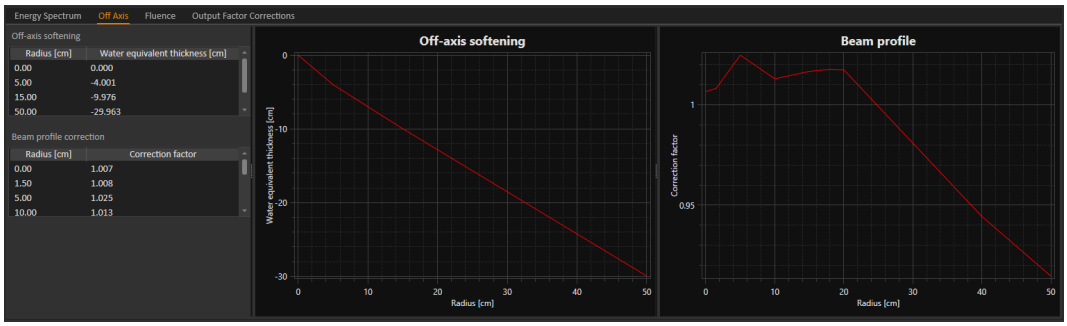


Figure 70. The Off Axis tab.

The off axis softening can be used to get better fits between profiles at both shallow and larger depths. If the general shape of the computed vs. measured profiles are good, but the quality of the fits change with depth, use the auto-modeling to adjust the off axis softening table to improve the models.

Beam profile correction

The fluence from the primary source is scaled with a rotationally symmetric profile, the Beam profile correction. The beam profile correction can be used to create a dip or an increase in the fluence intensity for small radii. It can also be used to create fall-offs at the corners, for instance to model the effect of the primary collimator or Elekta corner leaves. Note that the beam profile correction is only applied on the fluence from the primary source and not on the electron or flattening filter fluence.

Delete an entry by selecting it in the table and clicking **Delete**. Add a new entry by editing the boxes below the table and click **Add/Edit**. Change the Correction factor for the point at a given radii by marking the row in the table and editing the Correction factor in the box below the table, then click **Add/Edit**. Note that marking a row, changing the Radius and clicking **Add/Edit** creates a new entry and does not delete the originally selected value.

Beam profile corrections should be applied to improve the in-field fits between the measured and computed curves. Generally, parameters such as the flattening filters and source sizes should be

adjusted first. The beam profile correction table is then used to get a better agreement in the high dose region and at the shoulders.

WARNING!

Beam profile corrections and off-axis softening for radii larger than the largest field size cannot be evaluated using in-line and cross-line dose curves in beam commissioning. Values at radii larger than the largest field size influence the corners of the field directly but influence the x- and y-profiles only through phantom scatter. Therefore, the impact of beam profile corrections and off-axis softening cannot be reviewed for in-line and cross-line dose curves only. Diagonal profiles should be imported, or the Beam 3D module can be used to check the calculated dose of the entire field, including the corner, before commissioning. Be aware that manual adjustments of these two parameters are likely necessary for large radii when using auto-modeling. (530330)

4.3.4 Output factor corrections

The output factor corrections are part of the beam model and are adjusted to give a good fit to measured data at beam commissioning. Note that these are different from the measured output factors which are entered during dose curve import (*section 4.1.4 Output factors on page 99*). The measured output factors are only used to normalize the measured curves.

The output variation with field size is partly caused by phantom scatter and head scatter. The phantom scatter part is automatically part of the collapsed cone dose computation. The head scatter part is modeled using the flattening filter source.

In addition to these factors an explicit field size dependence is introduced with the output factor corrections. It corrects for factors such as backscattering into the monitor chamber, or model imperfections. The field measure computation used to transfer an arbitrary field into a square field is performed differently for different machines types. Refer to the *RSL-D-RS-9A-REF, RayStation 9A Reference Manual* for information on the field measure calculation.

Entries can automatically be added by clicking the **Sync field measures** button. The table will be populated with one field measure per imported field size and all correction factors will be set to 1. Note that existing field measures without corresponding measured curves will be deleted.

Alternatively, entries can be manually edited. Delete an entry by selecting it in the table and clicking **Delete**. Add a new entry by editing the boxes below the table and click **Add/Edit**. Change the Correction factor for a given Field measure by marking the row in the table and editing the Correction factor in the box below the table, then click **Add/Edit**. Note that marking a row, changing the Field measure and clicking **Add/Edit** creates a new entry and does not delete the originally selected value.

The output factor corrections can be normalized by clicking **Normalize correction factors**. This scales the Dose normalization with the output factor correction value at the reference field size and all output factor corrections with the inverse of that value.

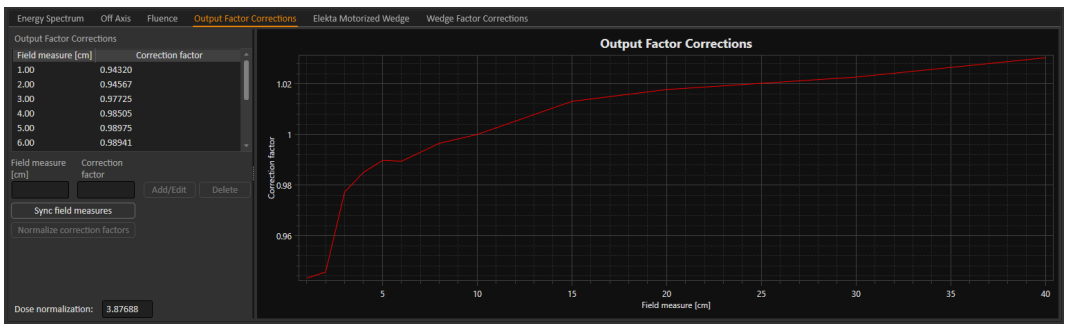


Figure 71. The **Output Factor Corrections** tab.

Output factor corrections are automatically computed during auto-modeling process. The "Output Factor Correction" step in auto-modeling should be run often, as changing other modeling parameters will cause the profiles to lose their normalization.

In general, for field sizes above 2x2 cm, the OF corrections should be close to 1.0. A "perfect" model would not require significant corrections, and thus this graph should be used to assess how good the model is. Variations of up to +/- 5% are not atypical. If the corrections are greater than this, additional modeling may be required. Usually, the output factor corrections increase with field measure.

Dose normalization

The dose normalization scales all dose computation with the given beam model. Note that an overall normalization can be hidden in the energy spectrum (when not normalized), in the output factor corrections (when not normalized) and partly in the beam profile corrections. There is no difference to the quality of the beam model where the normalization resides.

4.3.5 Physical wedges

Elekta Motorized and Standard wedges are both physical wedges and use a similar computation model. The wedge model acts as a modification of the open beam model by attenuating fluence, modifying the energy spectrum and adding a wedge scatter source.

All these effects are primarily determined by the wedge shape, described as the transmission through the wedge. It can be modified in order to obtain a good fit to measured dose curves.

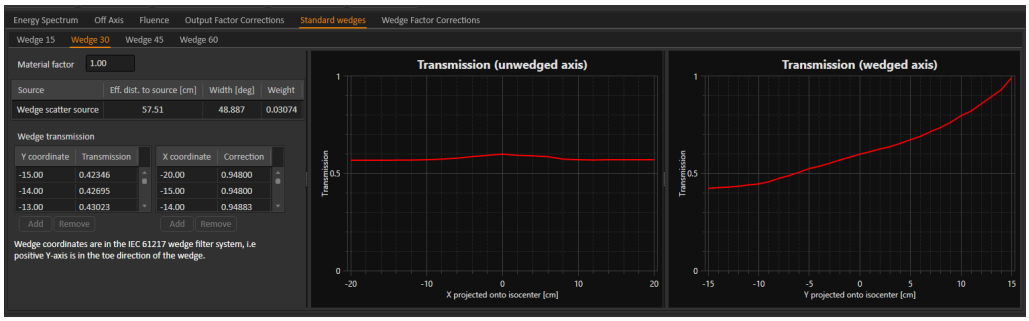


Figure 72. The Standard wedges tab.

For Standard wedges, clicking the **Add** button will add new entries with default values for coordinates and transmission/correction factors. Both coordinates and transmission/correction factors should be updated to the desired values.

The spectral changes are dependent on the thickness and material of the wedge as well as the energy of the incoming photon fluence. The water equivalent thickness of a wedge is computed from the transmission, using a mass attenuation coefficient for the mean energy in water. The energy and material dependent effects are then handled by the Material factor, which scales the water equivalent thickness of the wedge. For example, higher energies are less hardened when traversing the wedge. This is taken into account by reducing the Material factor.

The irradiated parts of a physical wedge will generate scatter fluence. This is described by the Wedge Scatter Source parameters. The scatter source is located at the Effective distance to source, affecting both how much is irradiated and the projection through any apertures. The Width (given in degrees) determines the standard deviation of the scattering angle, assumed to be normally distributed. Finally, the weight determines how much of the total fluence is comprised of wedge scatter.

Elekta Motorized wedge

For Elekta motorized wedges, the wedge shape is parameterized in x and y, corresponding to the perpendicular and wedged directions respectively (see *section 2.3.4 The wedge filter coordinate system on page 38*). The wedge transmission is given by

$$transmission = exp((q_1y^2 + q_2y^2 + q_3y + q_4)tan(p_1x^2 + p_2)) \quad \text{[Eq. 5]}$$

The rationale for this parameterization is that it resembles the physical shape of a motorized wedge, while giving enough flexibility to account for effects like beam divergence and spectral variations. The Elekta motorized wedge is an internal wedge situated above the MLC and jaws. This means that the irradiated part of the wedge is determined by the angle of the primary collimators as well as the effective distance to the source.

To commission a machine with an Elekta Motorized wedge, curves for the 60 degree wedge angle are required.

Standard wedge

For Standard wedges, the transmission along the y axis is given in coordinates specified by the user. Along the x axis, the user can specify a correction to the transmission along the y axis. The reason for this description is that standard wedges may not always be smooth in all regions.

The transmission of the wedge is displayed along the main axes. Outside of the specified coordinates, up to the maximum field size, the transmission is extrapolated with a constant value (shown as a dashed line).

A standard wedge is situated below the MLC and jaws. This means that the irradiated part of the wedge is determined by the segment shape and the effective distance to the source.

To commission a machine with Standard wedges, curves for all allowed wedge angles are required.

Details on wedge physics can be found in the *RSL-D-RS-9A-REF, RayStation 9A Reference Manual*.

Note: *Unlike other treatment planning systems, the physical shape of the wedge need not be specified in the Beam Commissioning tools. RayStation will use the measured curves to create an appropriate internal model to match the data.*

Note: *All scanned data for a wedge should be collected and imported using the same wedge orientation.*

4.3.6 Siemens virtual wedge

The MU distribution along the y axis for the Siemens Virtual wedge with angle **α** is described by

$$MU(y) = MU_{cax} \cdot exp(- \ c \cdot \mu \ (E) \cdot y \cdot tan(\alpha)) \quad \text{[Eq. 6]}$$

Here μ is the mean linear attenuation factor and c the calibration factor and MU_{cax} the MU at the central axis.

Siemens Virtual wedges are implemented to give the same dose at the center of the field as the open fields; therefore the wedge output factors entered by the user should be close to one. Imported wedged curves for Siemens Virtual wedge are optional but recommended before commissioning the machine.

Mean linear attenuation factor

The mean linear attenuation is entered per beam quality (energy level). The default value in the Beam Commissioning application is 0.002/ mm; this value should be obtained from the LINAC manufacturer.

Calibration factor

The calibration factor is entered per beam quality. It is a dimensionless calibration near 1 used to correct the wedge angle (see equation in *section 4.3.6 Siemens virtual wedge on page 154*). The default value in the Beam Commissioning application is 0.5; make sure to change this to the value obtained from the LINAC hardware manufacturer.

WARNING!

Siemens virtual wedge. The Siemens Virtual Wedge parameters, mean linear attenuation and calibration, should be adjusted from the default values to the proper values for your LINAC. Failure to do so may lead to error in the computed clinical dose. (508982)

4.3.7 Varian enhanced dynamic wedges

There are no beam model parameters except wedge factor corrections for Varian Enhanced Dynamic wedges. Imported wedged curves for Varian Enhanced Dynamic wedge are optional but recommended before commissioning the machine.

Note: *Varian Enhanced Dynamic wedges are only supported for beam qualities with dose computation energy 4, 6, 10, 15, 18 or 20 MV.*

4.3.8 Wedge factor corrections

The wedge factor corrections are used to obtain a better fit to measured data for different field sizes. The wedge factor corrections are analogous to the output factor corrections but affect only one wedge angle.

The wedge factor corrections are used as multiplicative factors when computing fluence for a wedged segment. The output of the segment is multiplied both by the output factor correction and the wedge factor correction for this field size. For the Varian Enhanced Dynamic Wedge and the Siemens Virtual Wedge the most open jaw configuration is used. The wedge factor correction is independent of wedge orientation.

Entries can automatically be added by clicking the **Sync field measures** button. The table will be populated with one field measure per imported field size and all correction factors will be set to 1. Note that existing field measures without corresponding measured curves will be deleted.

Alternatively, entries can be manually edited. Delete an entry by selecting it in the table and clicking **Delete**. Add a new entry by editing the boxes below the table and click **Add/Edit**. Change the Correction factor for a given Field size by marking the row in the table and editing the Correction factor in the box below the table, then click **Add/Edit**. Note that marking a row, changing the Field size and clicking **Add/Edit** creates a new entry and does not delete the originally selected value.

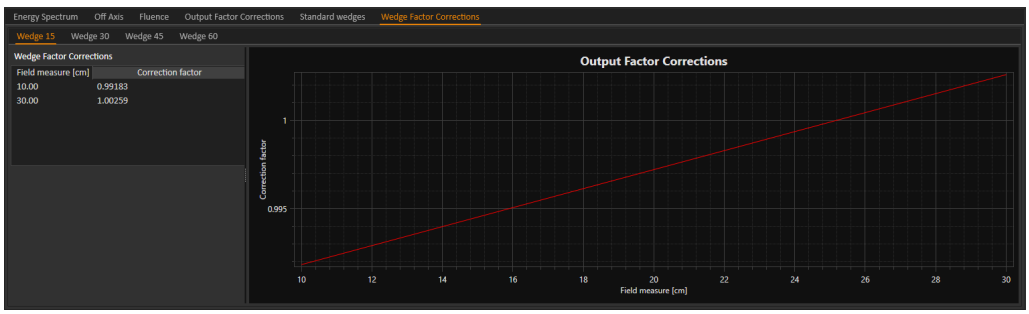


Figure 73. The **Wedge Factor Corrections** tab.

4.3.9 Cone factor corrections

Selecting a beam quality with cones will result in one additional tab, the Cone Factor Corrections tab.

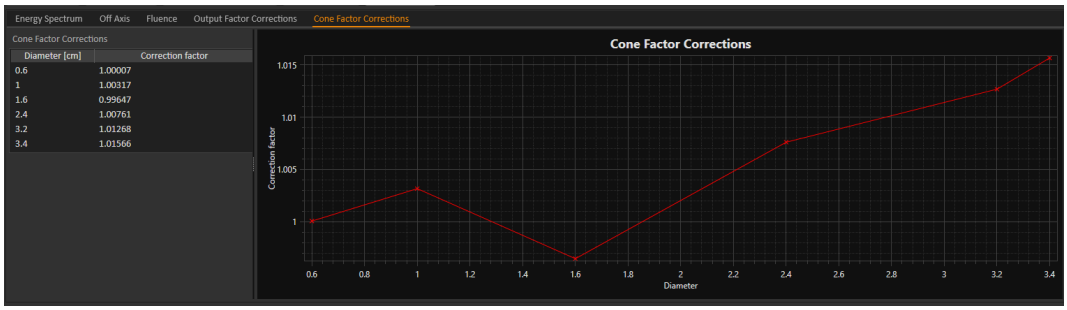


Figure 74. The Cone Factor Corrections tab.

For cone beam models, there are no specific beam model parameters except for the cone factor corrections. The cone factor corrections are analogues to the output factor corrections for the open fields. There must be a cone factor correction specified for all cones that have been added to the beam quality.

4.3.10 Summary of the beam model parameters

The beam model parameters are listed in the table below. Geometric parameters (not z) are defined at the projection onto the isocenter plane. Typical values are given in parenthesis.

Parameter	Description
Primary source • x width (0.05 cm – 0.3 cm) • y width (0.05 cm – 0.3 cm)	The width parameters specify the elliptical σ of the gaussian source intensity distribution at the source position.
Flattening Filter source • Effective Dist. to Sour. (6 cm – 15 cm) • Weight (0.05 – 0.1) • Width (1.0 cm – 3.5 cm)	The sum of the weights for the primary and the flattening filter source is always 1.0. The width parameter specifies the radial σ of the gaussian source intensity distribution at the source position.
Electron contamination • Weight of the source (0.005 – 0.01) • Width of the source (3 cm – 15 cm) • Weight of flattening filter electron source (0 – 1) • Energy spectrum parameters E0 (0 – 1) and C (0 – 1)	The width parameter specifies the radial σ of the gaussian source intensity distribution at the source position. The weight relates electron contribution to the photon contribution. The weight of the flattening filter electron source relates the secondary electron contribution to the total electron contribution. E0 and C describe the electron energy spectrum.
MLC • Effective Dist. to Sour. (different for different vendors, 30 cm – 55 cm) • Transmission (0.01 – 0.03) • Tongue and groove (0 cm – 0.1 cm) • Leaf tip width (0 cm – 0.5 cm) • Collimator calibration coefficients x (y for machines with MLC type set to Y) offset (0 cm – 0.1 cm), gain (0 – 0.01), curvature (0 [1/cm] – 0.001 [1/cm]), y (x for machines with MLC type set to Y) gain (0)	Multi leaf collimator. The tongue and groove effect is connected to the leaf side and the effective offset and width to the leaf tip. Tongue-and-groove, leaf-tip-width and collimator calibration coefficients are defined at the projection onto the isocenter plane.

Parameter	Description
X-jaws • Effective Dist. to Sour. (different for different vendors, 40 cm – 50 cm) • Transmission (0.001 – 0.1), (only for machines with MLC type set to X) • Collimator calibration coefficients x offset (0 cm – 0.1 cm), gain (0 – 0.01), curvature (0 [1/cm] – 0.001 [1/cm]	The jaws in the X direction according to the IEC61217 naming convention. The collimator calibration coefficients are defined at the projection onto the isocenter plane. The transmission of the X jaws is zero for a machine with MLC type set to Y.
Y-jaws • Effective Dist. to Sour. (different for different vendors, 20 – 50 cm) • Transmission (0.001 – 0.1), (only for machines with MLC type set to Y) • Position calibration coefficients y offset (0 cm – 0.1 cm), gain (0 – 0.01), curvature (0 [1/cm] – 0.001 [1/cm])	The jaws in the Y direction according to the IEC61217 naming convention. The transmission of the Y jaws is zero for a machine with MLC type set to X. Defined at the projection onto the isocenter plane. The collimator calibration coefficients are defined at the projection onto the isocenter plane.
Off Axis • Beam profile correction (0.95 – 1.05 in-field for flattened beams) • Off Axis softening (-30 – 0)	The beam profile correction is applied as an extra radially dependent scaling of the primary fluence. The radius is defined in the projection onto the isocenter plane. The off axis softening is given as the water equivalent geometric thickness, offset such that the thickness is zero in the center and otherwise negative. The radius is defined in the projection onto the isocenter plane.
Photon Energy Spectrum Fluence (0 – 0.1 if normalized)	Describes the energy spectrum of photons at the central axis at the isocenter plane.
Output Factor Corrections (0.95 – 1.05)	Normalize the beam monitor measurement to take field size variations into account. Found by a fit to measured output factors, is usually close to 1 for all field sizes.
Wedge shape (transmission) (0-1)	The wedge shape determines the attenuation of the wedge, the hardening of the energy spectrum and the wedge scatter contribution. Given as transmission fraction.

Parameter	Description
Wedge scatter source • Effective distance to source (dependent on type) • Width (10 - 20 degrees) • Weight (0.01 - 0.06)	The width determines the standard deviation of the scattering angle, assumed to be normally distributed. The weight determines the amount of scatter compared to the total fluence. The ratio between the primary and flattening filter source weights will be maintained.
Wedge factor corrections (0.95 - 1.05)	Normalize the beam monitor measurements to take the field size variations for wedged curves into account. Should be close to 1 for all field sizes.
Cone Factor Corrections (0.95 - 1.05)	Normalize the beam monitor measurement for cone fields to take field size variations into account. Found by a fit to measured output factors, is usually close to 1 for all cone sizes.

4.4 BEAM MODEL PARAMETERS FOR ELECTRONS

The electron beam model parameters are found on the beam quality level in the **Energy Spectrum** and **Source Phase Space** tabs. The **Energy Spectrum** tab have two sub-tabs; **Electrons** and **Contamination Photons**. The following sections describe the beam model parameters.

The name of the parameter is given first, then, if applicable, typical values in parentheses and then a description. For a full description and justification of the parameters, see *RSL-D-RS-9A-REF, RayStation 9A Reference Manual*.

In this section

This section contains the following sub-sections:

4.4.1	Energy spectrum	p. 162
4.4.2	Contamination photons	p. 163
4.4.3	Source phase space	p. 164

4.4.1 Energy spectrum

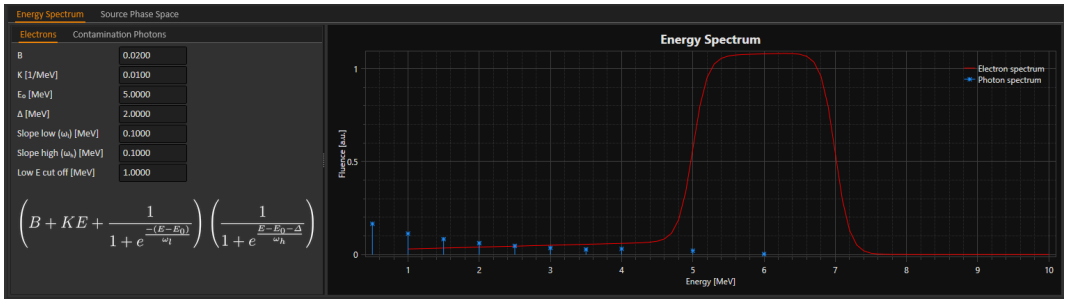


Figure 75. The **Energy Spectrum** tab showing the sub-tab **Electrons**.

The shape of the energy spectrum of the electrons as they escape the scattering foil is given by Equation 7.

$$\left(B + KE + \frac{1}{1+e^{\frac{-(E-E_0)}{w_l}}}\right)\left(\frac{1}{1+e^{\frac{E-E_0-\Delta}{w_h}}}\right) \quad \text{[Eq. 7]}$$

These parameters may be changed manually or by automatic optimization (**Optimize electron energy spectrum**).

Parameter	Description
B (0 – 5e^{-3})	The constant term in the linear low-energy tail.
K (0 – 5e^{-3} MeV^{-1})	The linear coefficient in the low-energy tail.
E_0 (near the nominal energy, MeV)	The location of the inflection point of the rising slope.
Delta, Δ (0.1 – 1.5 MeV)	The displacement between the inflection points of the rising and declining slopes. The width of the peak in the spectrum is controlled by Δ.
Slope low, w_l (0.1 – 0.8 MeV)	The steepness of the low-energy side of the peak.
Slope high, w_h (0.1 – 0.8 MeV)	The steepness of the high-energy side of the peak.
Low E cut off, E_{cut} (0 – 4 MeV)	The low energy cut-off. For energies below **Low E cut off**, Equation 7 is not used and the energy spectrum weight is set to zero.

4.4.2 Contamination photons

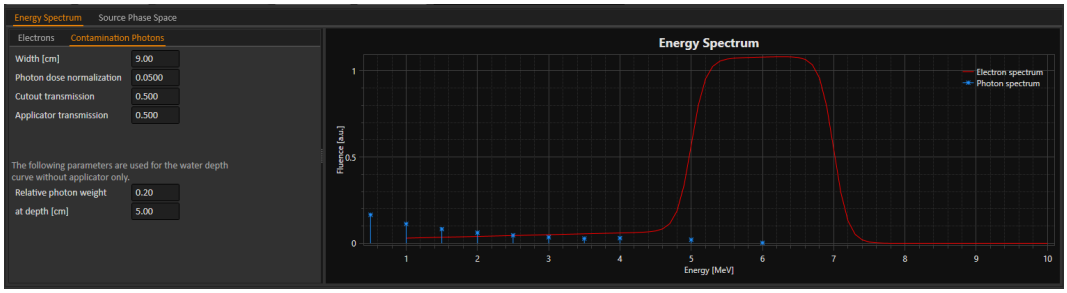


Figure 76. The **Energy Spectrum** tab showing the sub-tab **Contamination Photons**.

Parameter	Description
Width (5 cm - 15 cm)	The width (sigma) of the Gaussian which describes the contamination photon fluence.
Photon dose normalization (0.01 – 0.3)	A multiplicative factor scaling the photon contamination dose. This is not a relative weight. This factor is used for all applicator curves for the current beam energy.
Cutout transmission (0 – 1)	How much of the photon fluence passes through the cutout. Note that the value for cutout transmission cannot be obtained from the beam commissioning measurements alone but must be gathered from material specifications or supplementary measurements.
Applicator transmission (0 – 1)	How much of the photon fluence passes the applicator; only used for the case where there is no cutout. This factor is applied to the photon fluence outside the lowermost scraper layer opening.
Relative photon weight (0 – 1)	The amount of contamination photon fluence to be used when fitting the electron spectrum parameters to the open water depth dose curve. This parameter will be updated by the spectrum optimization.
At depth (5 cm - 10 cm)	The depth at which the relative photon weight is specified. This parameter will not be changed by the optimization.

4.4.3 Source phase space

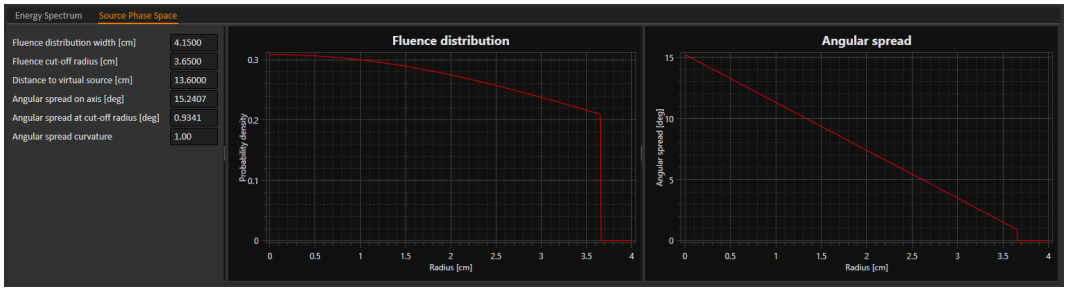


Figure 77. The **Source Phase Space** tab.

The following figure illustrates the electron source phase space parameters.

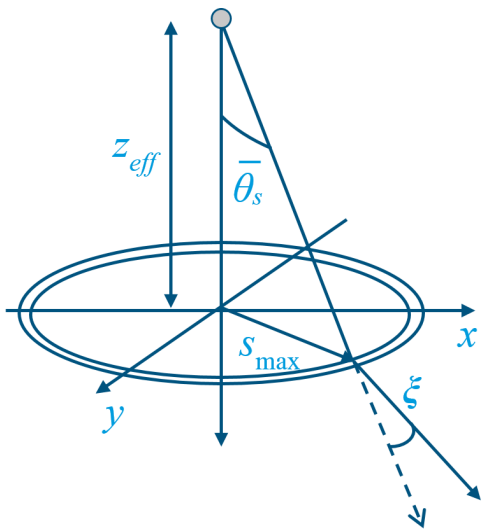


Figure 78. The electron source phase space parameters.

Parameter	Description
Fluence distribution width (2 – 5 cm)	The width of the Gaussian radial distribution of electrons at the source phase space plane (the secondary scattering foil).
Fluence cut-off radius (2 – 4 cm)	The extent of the circular disc from where the electrons appear to come. Denoted s_{max} in Figure 78.

Parameter	Description
Distance to virtual source (5 – 14 cm)	The distance between the source phase space plane and the virtual source point (from which the electrons appear to come). This parameter controls the average polar scattering angle of the generated electrons; the larger the distance to the virtual source, the more focused the electrons appear. Denoted z_{eff} in Figure 78.
Angular spread on axis (3 – 20 degrees)	The width (sigma) of the Gaussian distribution of polar angle smearing on axis. This distribution controls the spread of the electrons around the mean polar angle $\overline{\theta_s}$.
Angular spread at cut-off radius (0 – 8 degrees)	The width of the polar angle smearing at the cut-off radius.
Angular spread curvature (γ), see Equation 8.	For curvature = 1, the angular spread will be a linear function. For curvature < 1, the angular spread will approach the angular spread at cut-off radius faster with increasing radius. For curvature >1, the spread will approach the angular spread at cut-off radius slower with increasing radius. Typically, the angular spread at cut-off radius is smaller than the spread on axis.

The expression for the polar angle smearing

$$\sigma_\xi(s) = \sigma_\xi(s_{max}) + (\sigma_\xi(0) - \sigma_\xi(s_{max})) \left(1 - \left(\frac{s}{s_{max}}\right)^\gamma\right)^{1/\gamma}, \quad \text{[Eq. 8]}$$

where:

- s is the distance from the beam axis
- σ_ξ is the sigma of the Gaussian smearing applied on the angle of the electrons as they emerge from the source phase space plane
- $\sigma_\xi(s_{max})$ is the angular spread at cut-off radius

4.5 APPLICATOR PARAMETERS FOR ELECTRONS

Parameters for each applicator are found on the applicator level in three tabs; **Electron Applicator**, **Field Shaping Settings** and **Normalization**.

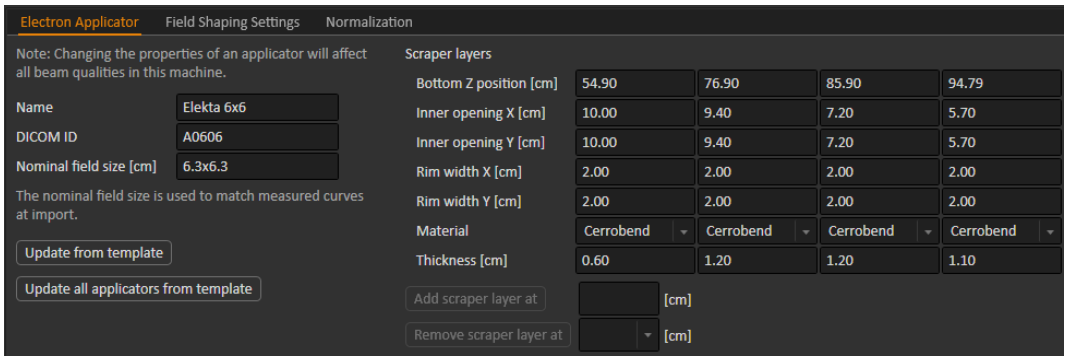


Figure 79. The **Electron Applicator** tab.

In this section

This section contains the following sub-sections:

4.5.1	Electron applicator settings	p. 167
4.5.2	Field shaping settings	p. 169
4.5.3	Normalization	p. 170

4.5.1 Electron applicator settings

The applicator settings are always defined in IEC 61217, regardless of selected jaw labeling standard and collimator coordinate system definition in the **General** tab.

The following general applicator parameters exist:

Parameter	Description
Name	The name used within RayStation to identify the applicator. The name must be unique within all applicators of a machine.
DICOM ID	Used in DICOM export as Applicator ID.
Nominal field size [cm]	The nominal field size without a cutout mounted. The nominal field size will be used when importing applicator curves to match the field size of the measured curves to the selected applicator.

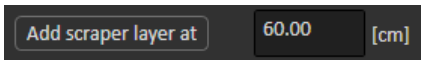
Per scraper layer, the following parameters exist:

Parameter	Description
Bottom Z position [cm]	Location along the beam line of the lowest (closest to the patient) edge of the scraper layer.
Inner opening X/Y [cm]	The extent of the opening in the scraper layer. These are the physical dimensions of the opening at the position of the scraper layer to be used for dose calculation. The opening is close to the physical dimensions of the applicator. However, differences between how scraper layers are defined in the RayStation applicator model compared to the physical applicator appearance may result in the inner opening to differ slightly compared to the physical dimensions. It is the final scraper layer that will affect the width of the computed profiles.
Material	The material the layer is made out of. Aluminum, Cerrobend and Yellow brass are supported materials.
Rim width X/Y [cm]	The width of the sides in the X/Y direction.
Thickness [cm]	The layer thickness.

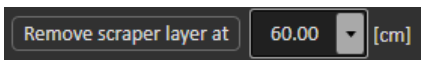
Note: *All applicators with the same name under different beam qualities are considered to be the same applicator. Changing an applicator parameter will change the applicator for all beam qualities for the machine.*

The applicator parameters can be updated from the corresponding template using **Update from template** or **Update all applicators from template** in case the template data have changed.

A new scraper layer can be added to an applicator by entering the value of the bottom Z position next to the **Add scraper layer at** button and clicking the button. This will add a scraper layer at the selected position with default parameters which can then be edited.



A scraper layer can be removed by selecting a bottom Z position in the **Remove scraper layer at** drop-down list and then clicking the button.



The bottom Z position of the last scraper layer is used for collision detection and should thus not deviate too much from the physical value.

4.5.2 Field shaping settings

The positions of the collimators as reported by the LINAC should be entered here. If the machine lacks backup jaw, the fixed y-jaw positions must be symmetric. For machines with backup jaw, the positions of both the x-jaw and y-jaw are usually symmetric.

The field shaping settings are always defined in IEC 61217, regardless of selected jaw labeling standard and collimator coordinate system definition in the **General** tab.

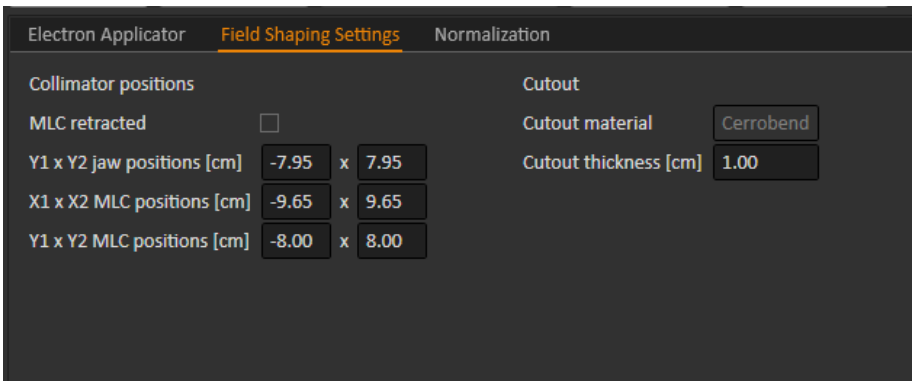


Figure 80. The **Field Shaping Settings** tab.

4.5.3 Normalization

Electron dose normalization is a multiplicative factor scaling the electron dose. This factor applies only to the current applicator (unlike photon dose normalization, see above).

Indirect electron weight correction factor affects the MC weight of scattered electrons. A value of 1.0 results in the default amount of scattering. A value of 2.0 effectively doubles the number of scattered electrons.

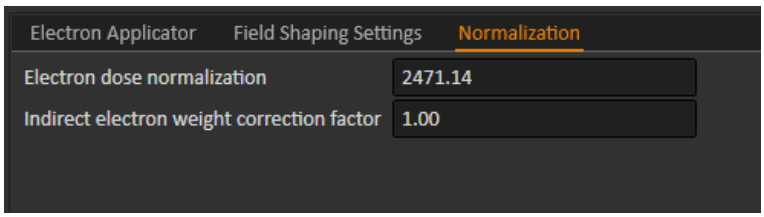


Figure 81. The **Normalization** tab.

4.6 AUTO-MODELING OF PHOTON BEAM MODEL PARAMETERS

Apart from manual adjustments, most users will want to fit the different beam parameters utilizing the auto-modeling tools. The auto-modeling proceeds as a list of consecutive steps where each step works on one set of parameters and keeps the other parameters fixed. For most steps, the set of parameters is limited to affect a certain region of depth or profile curves and affects a small number of parameters.

There are also two multi-parameter steps, one for the open model and one for wedge model. These steps optimize the fit between all regions of measured and computed curves simultaneously and work on a large number of parameters. It is recommended to start modeling by performing the multi-parameter step of the open model.

Since the result of a fit of a few free parameters depends on the value of the other fixed parameters, several iterations might be needed before the optimal parameter set is found. It is also important to have a good starting point, and to monitor the modeling so that it does not move in the "wrong" direction.

In this section

This section contains the following sub-sections:

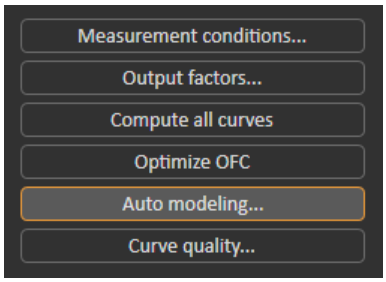
4.6.1	Launch auto-modeling	p. 172
4.6.2	Prerequisites for auto-modeling	p. 173
4.6.3	Prerequisites for output factor corrections auto-modeling	p. 174
4.6.4	The Auto Modeling dialog	p. 175
4.6.5	Auto-modeling steps	p. 178

Precautions

Note: *Review of parameter values after auto-modeling. The user must always review beam model parameter values after auto-modeling. The user must have proper training and be familiar with the beam model process. Results must be verified using professional standards of QA or alternative calculations.*

4.6.1 Launch auto-modeling

The auto-modeling workspace can be launched from the beam model workspace by clicking the **Auto-modeling…** button. The machine must be in edit mode.



The output factor corrections auto-modeling can also be launched by clicking the **Optimize OFC** button or by pressing Ctrl-W.

4.6.2 Prerequisites for auto-modeling

All machine geometry parameters must be correctly filled out and dose curves must be imported before the auto-modeling procedure can start.

Some optimization parameters can be changed after the model has been started but make sure to enter source-axis-distance, MLC leaf width, MLC and jaw constraints, reference field size and whether the machine has a fixed jaw or not. All of these factors significantly influence the dose computation.

The measurements that are needed are:

- absolute calibration factor
- curves
- output factors

For some beam model parameters reasonable starting points should be entered before auto-modeling begins. Enter collimator positions in the beam model workspace. Also enter collimator transmission and tongue-and-groove and leaf-tip geometry. Normalize the model as described in *section 4.8.2 Normalize the model on page 193*.

If the beam quality is modeled with respect to the photon Monte Carlo dose engine, statistical uncertainty must be set before modeling.

4.6.3 Prerequisites for output factor corrections auto-modeling

To be able to start the output factor corrections auto-modeling, it is not allowed to have any field measures in the output factor corrections list that are not among the measured curves.

It is also required that the smallest and largest field sizes among the measured curves have a corresponding field measure in the output factor corrections list. Use the **Sync field measures** button to populate the output factor corrections list with one field measure per imported field size and all correction factors set to 1. Refer to the *RSL-D-RS-9A-REF, RayStation 9A Reference Manual* for more information about field measures.

This applies also to auto-modeling with respect to photon energy spectrum and multi-parameter auto modeling, since output factor correction optimization is part of these steps as well. The same also applies to the wedge factor corrections list and auto-modeling with respect to wedge factor corrections.

4.6.4 The Auto Modeling dialog

The upper part of the **Auto Modeling** dialog contains a list of auto-modeling steps. A full set of steps can be loaded by clicking **Load template...**. A default auto-modeling workflow is delivered with the system, this might however not be the ideal workflow for your data. Steps can be added to the bottom part of the list, inserted at a selected position in the list and deleted from the list. Steps can also be moved up and down in the sequence. Any list of steps can also be saved as a template by clicking **Create template...**. Templates are accessible from any other PC that works with the same machine database. Note that templates are only saved when the machine (or CT) is saved to the database. It is possible to delete the default auto-modeling template. In that case it can only be recreated manually.

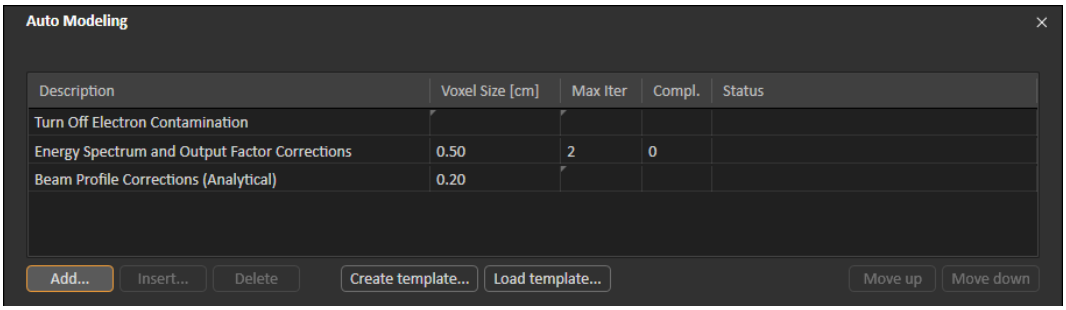


Figure 82. The upper part of the **Auto Modeling** dialog.

It is possible to set the computation resolution, the selected target curves and the maximum number of iterations for each step. The computation resolution and the maximum number of iterations can be set either when adding the step or by selecting a step and changing the Settings in the main window.

View or change the selected target curves by clicking the "**...**" button next to **Selected curves**.

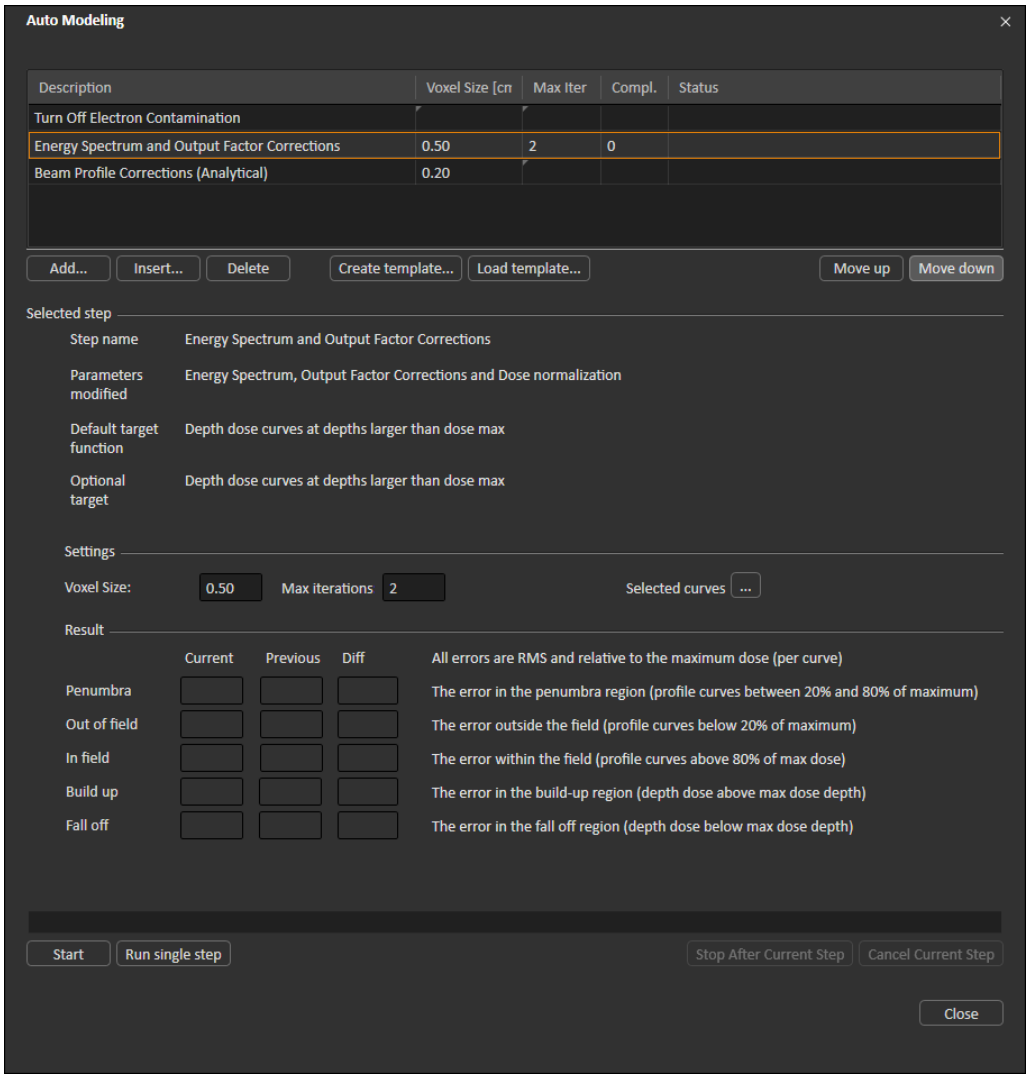


Figure 83. The **Auto Modeling** dialog.

Click **Start** to start the auto-modeling sequence. An optimization step includes calculating all dose curves with the selected resolution after finishing the optimization. For completed steps the root-mean square errors (RMS-errors) before and after the step are listed before (previous) and after the step (current) and the difference (after-before). In order to get accurate RMS-errors for the first step in an auto-modeling sequence, curves must have been computed before starting the auto-modeling.

The sequence can be stopped after the current step by clicking **Stop After Current Step**. The step execution can also be canceled during the current step by clicking **Cancel Current Step**. Run only one step by clicking **Run single step**.

Note: *Although using a coarser resolution will speed up the auto-modeling, most of the available modeling steps will suffer from the reduced quality. Be sure to use the appropriate resolution when selecting a step. Additionally, the size of the phantom can be adjusted (using the Measurement Conditions button) to better meet a particular need. For example, if the user wants to model the low dose region of a large field size, it may be necessary to adjust the phantom size to correctly calculate the dose.*

Note: *Auto-modeling of distributions such as beam profile corrections, off axis softening or output factor corrections are limited to the data points (radius or field measure) which define the distributions to begin with. A finer resolution in the description of the beam profile correction, off-axis softening or output factor correction can be obtained by adding extra points manually.*

4.6.5 Auto-modeling steps

There are three different types of auto-modeling steps: Optimization steps, Calculation steps and Modification steps.

Regions

The different auto-modeling steps operate on different target functions. The different regions for profile curves are the penumbra, the in-field and the out-of-field region (see *section 4.7 Curve quality on page 185* for more information about the different regions). The different regions for depth dose curves are the build-up (before the maximum dose) and fall off (below the maximum dose) region.

Table 4.1: Regions for depth dose curves.

	Build-up	Fall off
Open curves	Before maximum dose	Below the maximum dose
Wedged curves	Before maximum dose	Below the maximum dose

Table 4.2: Regions for profile curves.

	In-field	Out-of-field	Penumbra
Open curves	Dose > 80% of max dose for each curve.	Dose < 20 % of max dose for each curve.	Dose > 20% of max dose and dose < 80% of max dose for each curve.
Wedged curves	Inside the region defined by the sharpest gradients of the dose curve.	Outside the region defined by the sharpest gradients of the dose curve.	Not defined

Optimization steps

Each step affects a sub-set of beam model parameters which is to be included in the optimization while all other parameters are kept constant.

Since the result of a fit of a few free parameters depends on the value of the other parameters, several iterations might be needed before the optimal parameter set is found, not only within the same target set of parameters, but also back and forth between the different regions. The optimization algorithms thus are all iterative, and templates intending to model the beam as a whole should iterate between several regions in a reasonable manner.

The modeling will stop automatically if the optimal numeric solution is found or after the maximum number of iterations has completed for each modeling step. For both cases the system will keep the last iteration values as the new model parameters. If the optimization is started again the system will continue from the new position.

If the beam quality is modeled with respect to the photon Monte Carlo dose engine, mixed dose will be used for optimization. MC dose will be computed at the beginning and end of each step. While iterating, dose curves will be computed using the Collapsed Cone algorithm.

Auto-modeling step	Affected Parameters	Region	Default curves	Selectable curves
Electron Contamination [i]	Electron energy spectrum parameters ϵ_0 and c, primary electron source width and weight, additional electron source weight.	Build-up region from 2 mm depth to dose maximum.	Depth dose curves for the smallest, largest and reference field size.	All depth dose curves.
Energy spectrum and output factor corrections	Energy spectrum, output factor corrections and dose normalization.	Fall-off region.	All depth dose curves.	All depth dose curves.
Energy spectrum (parameterized) [ii]	Energy spectrum, output factor corrections and dose normalization.	Fall-off region.	All depth dose curves.	All depth dose curves.
Primary Source [iii]	Primary source widths in x and y.	Penumbra region.	All profiles for the smallest and the reference field size.	All profiles.
Flattening Filter Source [iv]	Flattening Filter Source width and weight.	Entire profile.	All reference field profiles.	All profiles.
Off Axis Softening [v]	Off axis softening water equivalent thickness.	In-field region.	All profiles for the largest field size.	All profiles.

Auto-modeling step	Affected Parameters	Region	Default curves	Selectable curves
Beam Profile Corrections [v]	Beam profile correction factors and dose normalization factor.	In-field region.	All profiles for the largest field size.	All profiles.
Output Factor Corrections [vi]	Output factor corrections and dose normalization factor.	Fall-off region.	All depth dose curves.	All depth dose curves.
Wedge Shape [vii]	Transmission along x and y.	In-field region.	All profiles for the largest fields size (one wedge).	All profiles (one wedge).
Wedge scatter source [vii]	Weight, size and effective distance to source of the wedge scatter source.	Entire profile.	All profiles (one wedge).	All profiles (one wedge).
Wedge Factor Corrections [vii]	Wedge factor corrections.	Fall-off region.	All depth dose curves (one wedge).	All depth dose curves (one wedge).

i Accurate data collection in this region is critical to a good fit.
ii The step is explained in detail in *Energy spectrum (Parameterized) on page 183*.
iii Re-selection may be necessary, especially if the smallest field data is of borderline quality.
iv Additional field sizes may be beneficial to add.
v If desired add extra points to the off axis softening distribution before, or after, optimization. Extra points are not added automatically.
Computation of dose curves with large fields can be influenced by the phantom size, if this is the case change the target curves to a smaller field size.
vi If desired, change the field measures in the output factor correction table before, or after, optimization. Additional field measures are not added automatically during optimization. It will not be possible to start the optimization if there are field measures in the table that do not correspond to the field size of any measured curve.
vii It is only possible to model data for one wedge angle at a time.

Multi-parameter optimization steps

Multi-parameter optimization uses a Gauss-Newton based optimization algorithm to simultaneously fit a large number of beam model parameters so that calculated curves match with measured curves. This algorithm uses a vector valued target function and typically converges after only a few iterations (5 to 10). The entire region of all selected curves are used in the target function, except for the first two millimeters of the depth curves.

The multi-parameter auto modeling step combines the parameters from all available separate steps for the open model in a simultaneous optimization.

The multi-parameter wedge auto modeling step is available for motorized and standard wedges. It affects wedge source and modulation parameters, wedge scatter corrections and the material factor.

If the beam quality is modeled with respect to the photon Monte Carlo dose engine, mixed dose will be used for optimization. MC dose will be computed at the beginning and end of each step. While iterating, dose curves will be computed using the Collapsed Cone algorithm.

Calculation steps

Instead of performing an iterative optimization some parameters can be calculated from the dose curves. Here curves are not target functions but rather they are the calculation input. As with the optimization steps the result of the calculations depend on other machine parameters.

Auto-modeling step	Affected Parameters	Region	Default curves	Selectable curves
Off Axis Softening (Analytical) [i]	Off axis softening water equivalent thickness.	In-field region.	Curves at different depths for the widest profile, where one curve is between 5 cm and 15 cm, and one profile is at depth 20 cm or deeper.	All profile curves. Only the widest profile that has one curve at a depth between 5 cm and 15 cm, and one curve at a depth of 20 cm or more, will be used.
Collimator parameters (Analytical) [ii]	Curvature, gain and offset for jaws and MLC.	Penumbra region.	All profiles.	All profiles.
Beam profile correction (Analytical) [iii]	Beam profile correction and dose normalization factor.	In-field region.	The shallowest curves of the widest profiles.	The shallowest curve of the widest profile can be exchanged by a profile for another field size, type or depth. If several curves of different profile widths are selected, only the widest profiles at the shallowest depth will be used.
Cone Factor Corrections	Cone factor corrections for all cone sizes.	Fall-off region.	All cone depth dose curves.	All cone depth dose curves.

i If desired add extra points to the off axis softening distribution before, or after, calculation. Extra points are not added automatically.
The step is explained in detail in *Analytical off axis softening calculation on page 183*.

ii The collimator parameters shift the collimator positions in clinical dose computation away from the nominal value (shown in beam lists, field sizes, Beam's Eye View and exported in DICOM). Review these parameters carefully before clinical use, in particular gain and curvature which give increasing shifts with increasing field sizes (*Collimator calibration on page 144*).
The step is explained in detail in *Collimator parameters calculation on page 183*.

iii If desired add extra points to the beam profile correction distribution before, or after, calculation. Extra points are not added automatically. The step is explained in detail in *Analytical beam profile correction calculation on page 183*.

Modification steps

The modification steps change a set of parameters to a predefined value.

Auto-modeling step	Affected Parameters	Calculation input	Comment
Turn off electron contamination	Electron weight and flattening filter weight are set to 0.	N/A	Used to remove effects of electron contamination before an auto-modeling of the energy spectrum is performed.

Target function of auto-modeling optimization

The target function of the auto-modeling fit is the sum of the squared differences between measured and computed dose points.

$$x^2 = \sum_c \sum_i (m_i^c - c_i^c)^2 \qquad \text{[Eq. 9]}$$

The index is run over the data points in one curve and c are the different curves (depth-dose curves or profiles). Since it is a sum over dose points, curves which are sampled at a high frequency are given a higher weight in the optimization.

Target function of multi-parameter auto-modeling optimization

The target function of the multi-parameter auto modeling is a vector function $f = (f_1, f_2, ..., f_n)$ where the number of components n is equal to the total number of measured dose points for all selected curves. Each component f_j is a weighted difference between measured m_j and computed c_j dose value

$$f_j = w_j(m_j - c_j)^2 \qquad \text{[Eq. 10]}$$

where the weights w_j are inversely proportional to the central finite difference of the measured curve at position j. The weights are normalized so that larger profile curves are weighted higher in the optimization. Depth curves are considered most important and are given a total weight two times higher than the profile curve of maximum field size.

Energy spectrum (Parameterized)

The auto-modeling step Energy spectrum (Parameterized) optimizes the energy spectrum, output factor corrections and absolution calibration, but differs from the non-parameterized version by forcing the particle fluence spectrum with energy to follow the shape

$$F(E) = E^{(c1-1)} \cdot e^{(-c2 \cdot E)} \quad , \qquad \text{[Eq. 11]}$$

where F(E) is the particle fluence for energy E.

$$C1 = E_{average}/(E_{average} - E_{mostprobable}) \qquad \text{[Eq. 12]}$$

$$C2 = 1/(E_{average} - E_{mostprobable}) \qquad \text{[Eq. 13]}$$

Note that this is the particle fluence energy spectrum corresponding to the energy fluence energy spectrum cited in paper *Fippel (1999) from Ali E. S. M. and Rogers D. W. O., Functional forms for photon spectra of clinical linacs, Phys. Med. Biol. 57 (2012) 31-50.*

Analytical off axis softening calculation

This algorithm requires at least two profile curves of the same field size where one is measured at a depth between 5 and 15 cm and the other deeper than 20 cm.

The algorithm works like this:

1. Calculate the ratio between the two computed curves for different water equivalent depths (using no off-axis softening).
2. Calculate the ratio between the two measured curves.
3. Sets the Off Axis Softening to the water equivalent depths so that the ratios are the same.

To get a good result it is important to have many off axis softening data points predefined.

Analytical beam profile correction calculation

The algorithm works like this:

1. Set the Beam Profile Corrections to 1 for all radii.
2. Compute the ratio between the measured and the computed curves in the infield region for the different radii.
3. Set the Beam Profile Corrections to the ratios.

To get a good result it is important to have many Beam Profile Corrections data points predefined.

Collimator parameters calculation

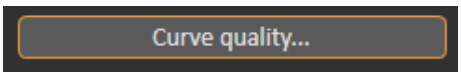
The algorithm works like this:

1. Calculate the width of all measured and computed profiles at half the maximum dose for the curve.
2. Rescale the widths to isocenter.
3. Adapts a first-degree polynomial with the offset, gain and curvature as coefficients and the field edge offset as variable using the widths of the computed for X and Y.
4. Sets the collimator parameters to the polynomial coefficients.

If the curves were collimated with MLC retracted, only jaw parameters can be adjusted. If the machine was a fixed jaw machine or the fields were collimated with only MLC, the MLC parameters can be adjusted. It is not possible to run this step with both MLC and jaw collimated fields.

4.7 CURVE QUALITY

At any point, when there are computed curves, the curve quality for the selected curves can be viewed by opening the **Curve quality** dialog. The fit quality in different regions can also be seen as an overall measure in the **Auto Modeling** dialog.



In this section

This section contains the following sub-sections:

4.7.1	Measured curve quality	p. 186
4.7.2	Fit quality	p. 188

4.7.1 Measured curve quality

The curve quality is computed for measured curves. The flatness and symmetry are calculated within the flattened region according to the IEC 60976 standard. The size of the flattened region is the FWHM minus an offset which depends on the field size according to the table below (see also Figure 85). The offset is not defined by IEC 60976 for field sizes smaller than 5 cm, but in the Beam Commissioning module the offset is zero for field sizes smaller than 4 cm.

Field size (cm)	Offset (cm)
< 4	0
4 - 10	1
10 - 30	0.1 * field size
> 30	3

For wedged curves in a wedge direction, the concept of flatness and symmetry does not have a relevant meaning and is not presented. The penumbra in the low-dose region can also be difficult to assess and is therefore not presented either.

Penumbra width

The penumbra is defined as the region where the dose is between the 20% and 80% of the maximum dose of the curve.

$$P = |x_{80\%} - x_{20\%}| \qquad \text{[Eq. 14]}$$

Symmetry

Symmetry is a measure of the maximum ratio between two dose points D(x) spaced symmetrically about the central axis.

$$S = max\left(\frac{D_x}{D_{-x}}, \frac{D_{-x}}{D_x}\right) - 1 \qquad \text{[Eq. 15]}$$

Symmetry is displayed for all field sizes.

Flatness

Flatness is a measure of the largest deviation of the flattened profile from the maximum dose of the entire profile.

$$F = \left(\frac{D_{max}}{D_{min}}\right) \qquad \text{[Eq. 16]}$$

Flatness is displayed for field sizes > 4 cm.

4.7.2 Fit quality

For depth dose curves a fit quality is computed in the build-up and fall-off region. The build-up region is the region between the surface and the depth where maximum dose has been reached. The fall-off region is the entire region outside the build-up region.

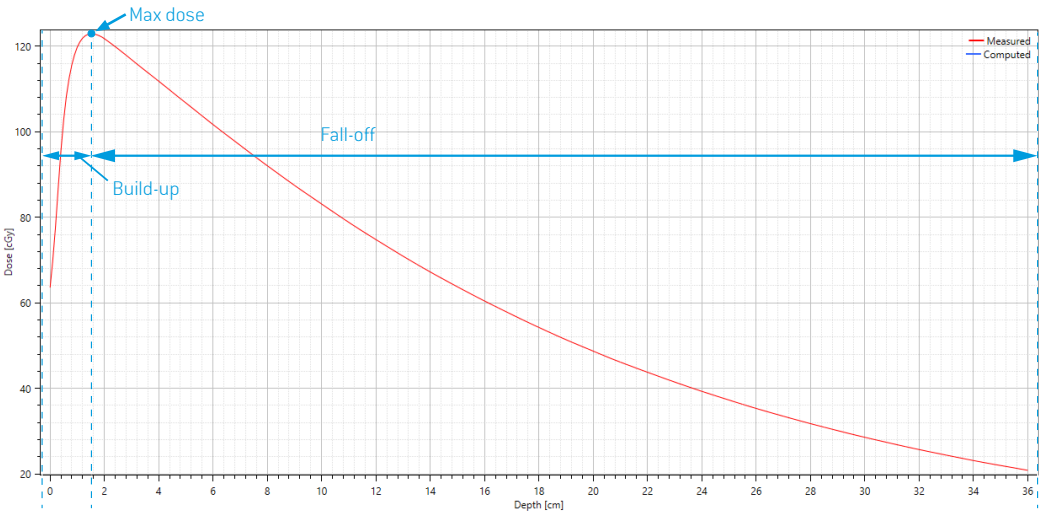


Figure 84. The depth dose curve with build-up and fall-off definitions.

For open field profiles a fit quality is computed in the out-of-field, in-field and penumbra regions. The in-field region is the region between the left and right penumbra, as defined by the penumbra width. The out-of-field region is the region outside the penumbra.

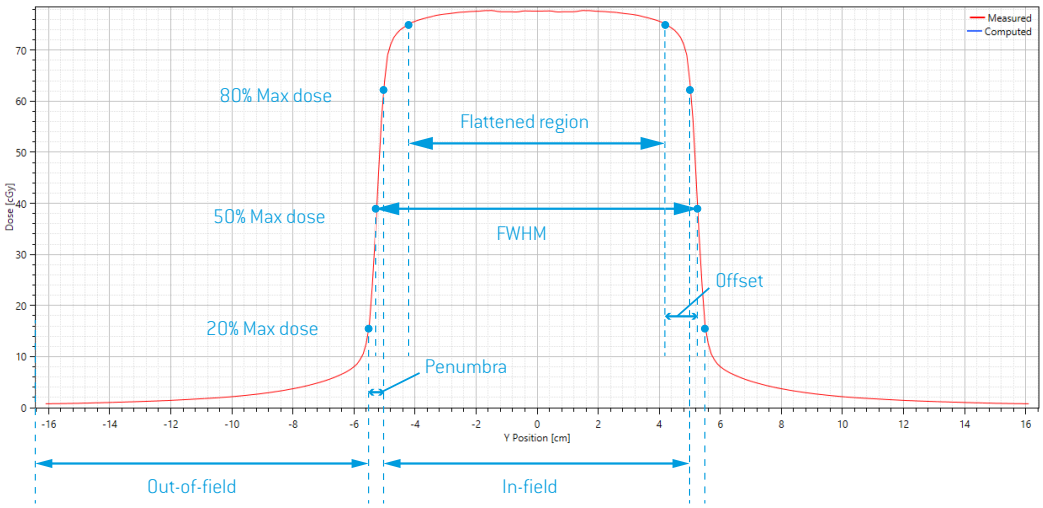


Figure 85. A profile dose curve with in-field, out-of-field, penumbra regions and FWHM (full width at half maximum) as well as the flattened region used for symmetry and flatness. The offset value depends on the field size and is calculated according to IEC 60976.

For wedges the in-field region is defined as the region between the points where the penumbra is sharpest. All other points are part of the out-of-field region.

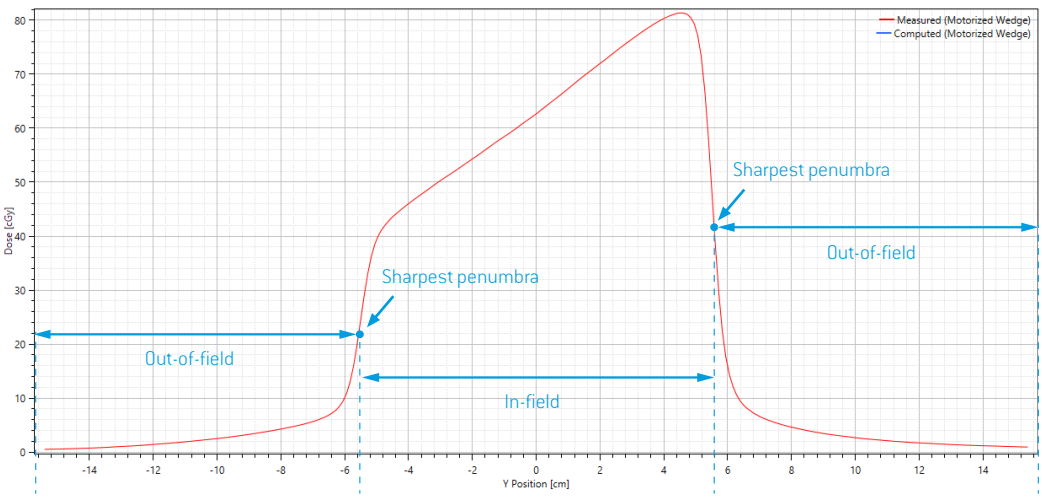


Figure 86. Dose regions for a wedged profile.

The fit quality is the root-mean-square difference between a computed and a measured curve. For each curve and region the RMS (Root Mean Square) is calculated by taking the square root of the average squared error between the computed curves and the measured curves

$$RMS = \sqrt{\frac{1}{N}\sum_{i=1}^{N}\left(\frac{computed\ dose - measured\ dose}{maximum\ dose\ for\ measured\ curve}\right)^2} \quad \text{[Eq. 17]}$$

where N is the number of points of the curve in the relevant region. The **Auto Modeling** dialog averages the build-up difference over all curves after taking the RMS for each curve.

4.8 HOW TO CREATE A PHOTON BEAM MODEL

This section gives advice on how to reach a good machine model.

In this section

This section contains the following sub-sections:

4.8.1	Steps before photon beam modeling	p. 192
4.8.2	Normalize the model	p. 193
4.8.3	Resolution	p. 194
4.8.4	Uncertainty	p. 195
4.8.5	Flattening filter free beam model	p. 196
4.8.6	Fit the model parameters to the measured data	p. 199
4.8.7	Tips and tricks	p. 209
4.8.8	Common problems and solutions	p. 211

Precautions

WARNING!

Beam model parameters. The accuracy of the dose computation depends critically on the beam model parameters established during beam commissioning. Before a machine is commissioned, all beam model parameters must be carefully reviewed by a person with proper training. (508983)

4.8.1 Steps before photon beam modeling

The first steps involved in creating a new machine model are outlined below. The details of each step are described in other sections.

1. Copy an existing machine (Template, Commissioned, Uncommissioned or Deprecated) by right clicking on the machine and selecting **Copy**. Choose a machine as similar as possible to the one you are about to commission regarding for example collimator properties.
2. Enter **Edit mode** for the copied machine.
3. Change the name of the machine in the **General** tab, optionally enter comments, and edit the static machine properties and optimization parameters described in *section 4.2 Machine properties on page 110*.
4. If the machine has the wrong beam quality, create a new beam quality by right-clicking the machine in the tree view and selecting **Add new beam quality**. Then delete the old beam quality by right-clicking the energy level in the tree view and selecting **Delete beam quality**.
5. If the copied machine has measured curves, delete the curves as described in *section 4.1.1 Delete curves on page 89*.
6. Enter the SSD of the measured curves and the absolute calibration point as described in *section 4.1.6 Absolute dose calibration point on page 105*.
7. Import open field curves as described in *section 4.1.2 Import curves on page 90*.
8. Enter known geometric information such as collimator positions and transmissions.
9. If there are large deviations between measured and computed curves at this step, normalize the model as described in *section 4.8.2 Normalize the model on page 193*. If there are small deviations, the model is automatically normalized at auto-modeling.
10. Work on open field parameters using auto-modeling (*section 4.6 Auto-modeling of photon beam model parameters on page 171*) or manual tuning.

Note: *A LINAC model machine is commissioned for all beam qualities (energy levels) as well as open and wedged fields simultaneously. To start clinical treatment with one beam quality (energy level), create a machine with only one beam quality and no wedges and commission it. Then copy this machine and work on an un-commissioned version under another name. When the new machine with wedges, or several energy levels, is ready for clinical introduction deprecate the old machine, rename the new machine model and commission it.*

4.8.2 Normalize the model

To set the normalization of the beam model perform these steps:

- normalize the energy spectrum (See *Photon energy spectrum on page 146*)
- normalize the output factor correction (See *section 4.3.4 Output factor corrections on page 150*)
- compute all curves

Note the computed dose in the reference point and the measured dose in the reference point. Multiply the normalization factor with reference dose divided by computed dose. When computing the depth dose curve for the reference field after this change the values should agree in the reference point.

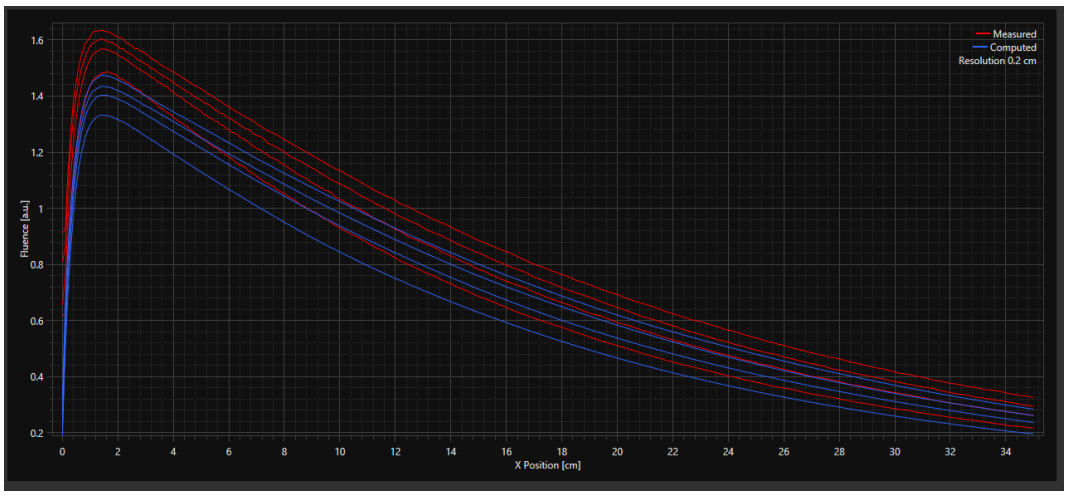


Figure 87. The depth dose curve.

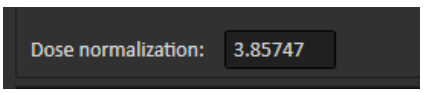


Figure 88. The Dose normalization field in the **Output Factor Corrections** tab.

4.8.3 Resolution

Collapsed cone beam models

The computation resolution is specified for the density grid and TERMA grid. The same resolution is used in the x, y and z direction. The TERMA is computed for the full phantom volume (specified by the phantom size described in *Phantom size on page 101*) and dose is calculated in each measurement point for all measured curves. A low resolution speeds up the computation during auto-modeling and dose curve computation. But a low resolution TERMA grid also gives discretization uncertainties in the photon dose which must be remembered when comparing measurement and computation. The electron part of a curve is not influenced by the resolution.

A resolution of 0.4 cm can be enough to get the coarse model parameters right. For fine tuning 0.2 cm is more suitable.

Monte Carlo beam models

The computation resolution is specified for the density grid. The same resolution is used in the x, y and z-direction. Dose is computed in all voxels in the phantom and then interpolated in each measurement point for all measured curves.

4.8.4 Uncertainty

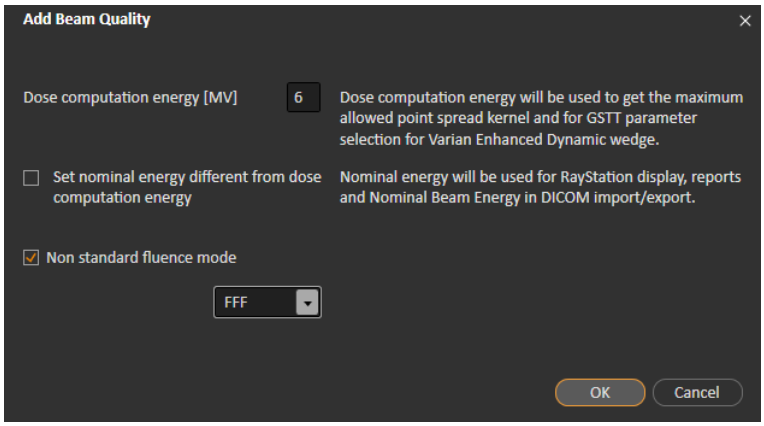
Each field will be computed until the computation uncertainty is reached. A higher uncertainty can be used to speed up dose curve computation and auto-modeling. For fine tuning a lower uncertainty is required. This is only visible for Monte Carlo beam models.

4.8.5 Flattening filter free beam model

If the beam quality to be modelled is flattening filter free, perform the following steps:

1 – Non-standard fluence mode FFF

Select non standard fluence mode **FFF** when adding the new photon beam quality. Note that it is not possible to change the fluence mode after the beam quality has been created. This will ensure correct settings in the DICOM export.


Add Beam Quality
Dose computation energy [MV]
6
Dose computation energy will be used to get the maximum allowed point spread kernel and for GSTT parameter selection for Varian Enhanced Dynamic wedge.
Set nominal energy different from dose computation energy
Nominal energy will be used for RayStation display, reports and Nominal Beam Energy in DICOM import/export.
Non standard fluence mode
FFF
OK
Cancel

WARNING!

Non-standard fluence mode. When modelling a photon beam quality with non-standard fluence mode (FFF/SRS), it is essential to select the correct fluence mode when adding the beam quality. If the fluence mode is not set correctly, plans using the beam quality may be misinterpreted by the LINAC, leading to incorrect delivered dose.

If standard fluence mode is used for the beam quality, RT Plans will set Fluence mode to "STANDARD" and the Fluence mode ID is not exported.

If non-standard fluence mode is selected, RT Plans will set Fluence mode to "NON_STANDARD" and the Fluence mode ID to the selected fluence mode (FFF/SRS). (508990)

2 – Off-axis softening

Set all entries in the **Off-axis softening** table in the **Off Axis** tab to zero. The off-axis softening models the change in energy spectrum off axis due to the flattening filter. As the effect of the off-axis softening is not present for a flattening filter free beam quality, all entries in the table should be close to zero.

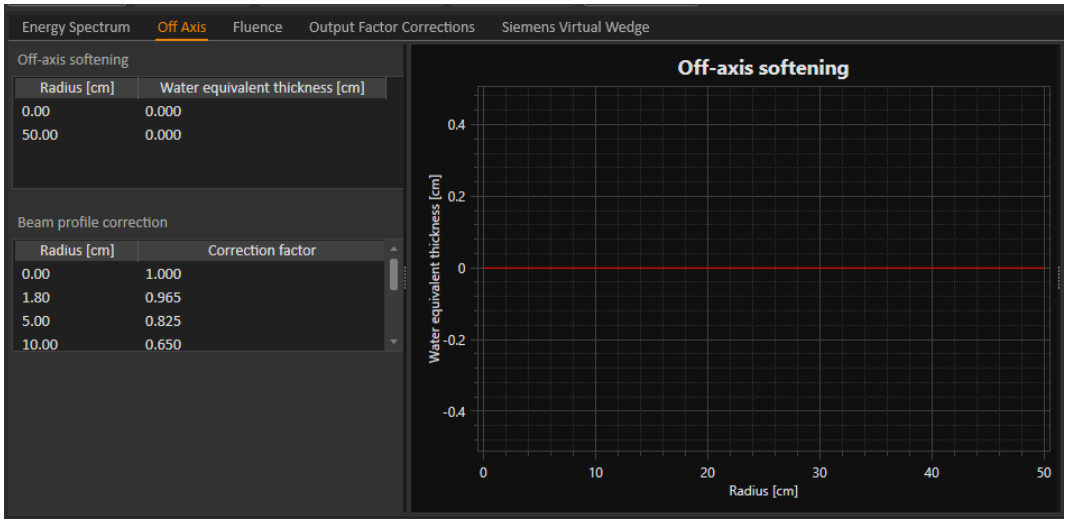


Figure 89. The Off-axis softening table with the entries set to zero.

3 – Beam profile correction

Use the **Beam profile corrections** to model the correct, non-flat, shape of the flattening filter free profiles in field. The auto modeling will only affect values at radii corresponding to 95% of the maximum field size. Points at larger radii should be manually adjusted.

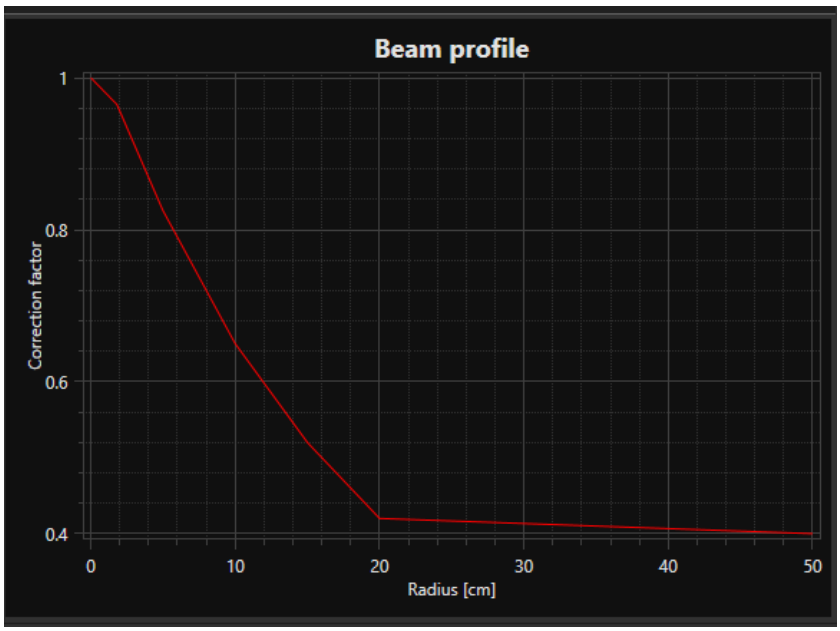


Figure 90. Beam profile correction for a flattening filter free profile.

4 – Flattening filter sources

Looking at the sources in the **Fluence** tab, the weight of the flattening filter photon source can usually be reduced compared to a beam model with flattening filter. However, the flattening filter photon source is also the source of general photon scatter. Hence, it may be necessary to keep a smaller weight on the flattening filter photon source in order to get the correct modeling of scatter out of field. The correct parameter values must be set based on comparison to the measured curves. The same reasoning applies to the flattening filter electron source.

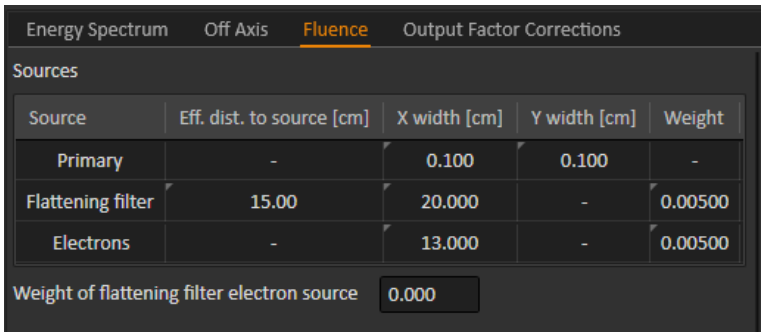


Figure 91. Example sources for a flattening filter free beam quality.

4.8.6 Fit the model parameters to the measured data

WARNING!

Beam model parameters. The accuracy of the dose computation depends critically on the beam model parameters established during beam commissioning. Before a machine is commissioned, all beam model parameters must be carefully reviewed by a person with proper training. (508983)

General advice

The goal of the beam commissioning procedure is to find beam model parameters which give the best fit of computed curves to measured data. These are a few general advices to keep in mind.

- Different auto-modeling modes might have to be repeated in turn and manual adjustments may also be necessary.
- Curves should be regularly recomputed during the commissioning to verify the progress.
- The Output Factor Corrections auto-modeling mode can be repeated between most other steps, or when the absolute level match is not good enough between the measured and computed curves.
- If the size of the measurement detector is not described correctly in the measurement conditions, differences between measured and computed curves that originate in measurement resolution might be incorrectly corrected for by other parameters.

A step-by-step instruction for beam commissioning using multi-parameter optimization

Step 1 – Perform the steps which are prerequisites for auto-modeling

The steps are described in *section 4.6.2 Prerequisites for auto-modeling on page 173*.

Step 2 – Multi-parameter optimization

It is recommended to start modeling with multi-parameter optimization of the open model.

Step 3 – Auto-modeling and manual adjustments

Use the separate auto-modeling steps or manually tune the model for dose curve regions where the fit is not satisfactory. The penumbra and out-of-field region of beam profile corrections will not be affected by auto modeling and must always be manually adjusted. Use the Beam 3D module to correctly tune these values for large radii affecting corner dose of the largest field size.

A step-by-step instruction for beam commissioning using auto modeling steps for separate dose curve regions

Step 1 – Perform the steps which are prerequisites for auto-modeling

The steps are described in *section 4.6.2 Prerequisites for auto-modeling on page 173*.

Step 2 – Remove electrons

The photon energy spectrum is determined from the depth dose curves. To avoid electron contamination in the first steps, open the **Auto Modeling** dialog by clicking the **Auto Modeling…** button followed by **Add...**. Select **Turn Off Electron Contamination** from the menu. Depending on the measured curve data, sometimes a better result is achieved by keeping the electron model from the template and continue auto-modeling from there.

If the lowest energy bin in the photon energy spectrum (0.5 MeV) becomes very large when auto-modeling with respect to the photon energy spectrum with the electrons turned off, this may indicate that low energy photons are used to get build-up dose instead of electrons. If this happens, electrons should be turned back on again. Manually reduce the low energy bin again.

The electrons are not as important for smaller field sizes as for larger field sizes. Therefore, it is possible to try auto-modeling the photon energy spectrum only for field sizes up to approximately the reference field size with the electrons turned off.

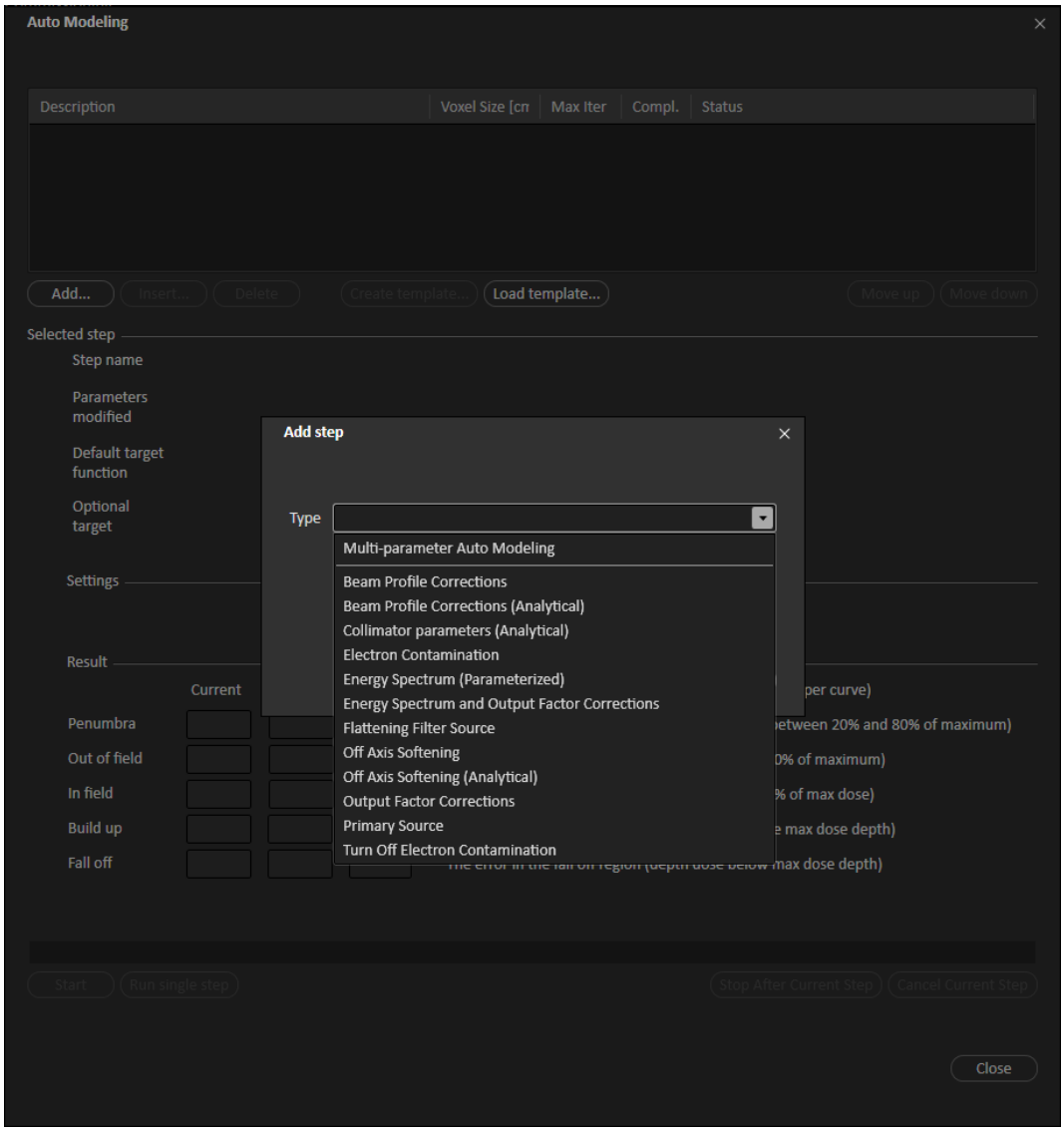


Figure 92. The **Auto Modeling** dialog.

Step 3 – Output Factor Corrections auto-modeling

To get the absolute dose level between the measured and computed curves to match better, perform auto-modeling with respect to **Output Factor Corrections**. Before starting, open the **Output Factor Corrections** tab and look at the field measures present in the table. It is not necessary to have all field measures of the measured curves present, but the field measures chosen in the table should be present among the measured curves otherwise the auto-modeling will not start. Use the **Sync**

field measures button to populate the output factor corrections list with one field measure per imported field size.

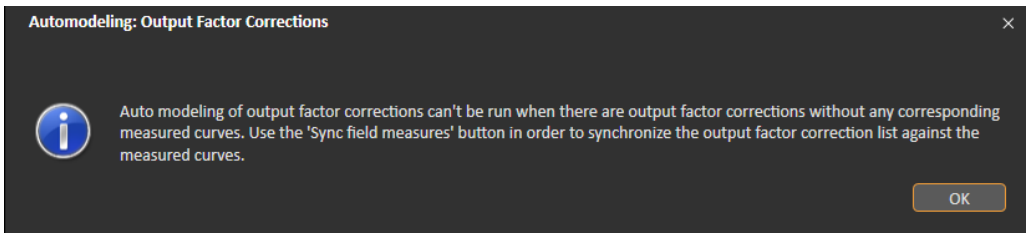

Automodeling: Output Factor Corrections
Auto modeling of output factor corrections can't be run when there are output factor corrections without any corresponding measured curves. Use the 'Sync field measures' button in order to synchronize the output factor correction list against the measured curves.
OK

Figure 93. An error message is displayed when there are no corresponding measured curves present.

The full range from the smallest to the largest field measure among the measured curves should be covered in the output factor correction list. Remember that dose computation using field sizes that are smaller or larger than the measured curves are not bound by measurement and can be erroneous. Rectangular or irregularly shaped segments are converted to square fields through the field measure (please refer to the *RSL-D-RS-9A-REF, RayStation 9A Reference Manual* for further information).

The auto-modeling will not add new field measures. To add new field measures, select the field **Field measure** and input the correction factor in the corresponding field and click the **Add/Edit** button. To delete a field measure, click **Delete**.

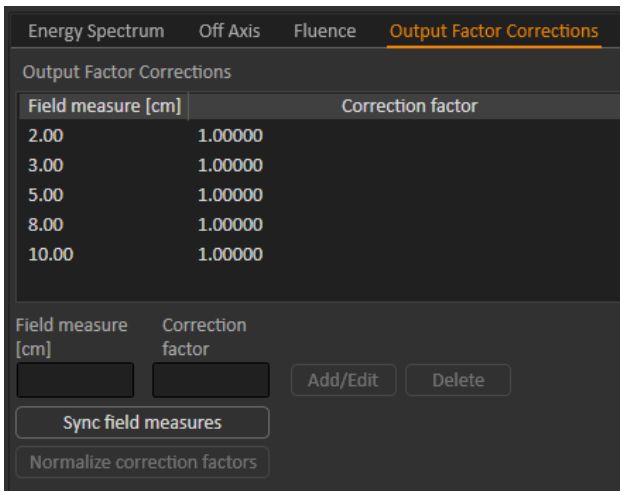


Figure 94. The Output factor corrections tab.

Usually the output factor corrections increase with increasing field measure, at a level of a few percent. If the output factor corrections deviates more than a few percent from each other at the end of the modeling, there is reason for suspicion, in that case one may need to change the flattening filter weight or width.

Note: *The field measures of the output factor correction (smallest to largest) should cover the field sizes that the beam model is expected to calculate on. Extrapolation towards smaller or larger values than what is present in the table assumes a constant output factor, for smaller field the same as for the smallest field in the table, for larger fields the same as for the largest field in the table. To obtain a different behavior add extra points to the output factor correction table. Remember that auto-modeling using field measures that are smaller or larger than the measured curves is not possible. If extra field measures are added these should be verified by other measurements than the curves in beam commissioning.*

Step 4 – Photon energy spectrum auto-modeling

Perform an auto-modeling with respect to Energy Spectrum and Output Factor Corrections. The photon energy spectrum is made out of discrete bins (default is 10 bins for a 6 MV spectrum) and the fit is performed using depth dose curves as target functions. After the fit the measured and computed depth dose curves should match fairly well below D_{max} to the deepest measured depth, otherwise redo the previous steps. Sometimes it is hard to get a perfect match for the largest field sizes (approximately larger than 30 x 30 cm^2) depending on the energy and measurement conditions. The photon energy spectrum auto-modeling does not always give physically reasonable results since it is only trying to fit the sum of the squared differences between measured and predicted dose and has no knowledge of what is a physically reasonable energy spectrum. To constrain the auto-modeling towards physically feasible shapes use the auto-modeling step Energy spectrum (Parameterized) described in *Energy spectrum (Parameterized) on page 183*.

If necessary, tune the photon parameters manually or by repeating the auto-modeling modes. To manually change the photon parameters select the energy to be adjusted from the Energy [MeV] list and enter the new fluence in a.u. in the **Fluence [a.u]** field. The spectrum will be normalized automatically if the **Normalize on Add** checkbox is checked. The spectrum can also be normalized manually once all the values are edited by clicking the **Normalize spectrum** button. When satisfied with the depth dose curves below D_{max}, turn to the electron parameters.

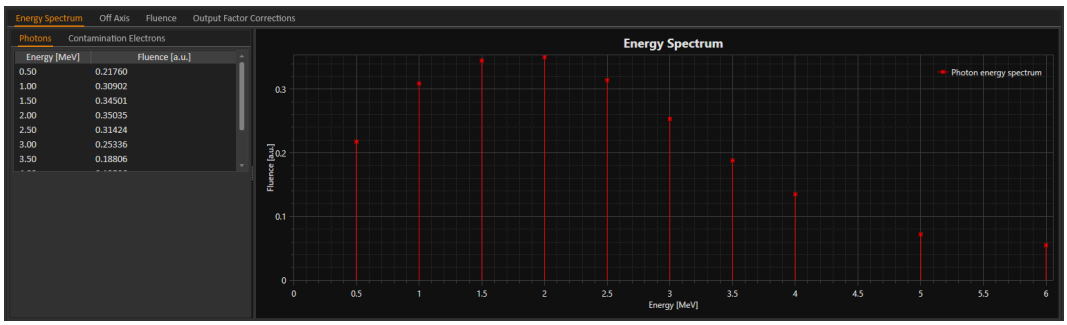


Figure 95. The Energy spectrum tab.

Step 5 – Electron contamination auto-modeling

The electron parameters are determined from the depth dose curves closer to the surface than dose maximum, D_{max}. A reasonable start guess is to set the Electron energy model parameter E0 = 1 and

C = 0 (**Energy Spectrum** tab, **Electrons** tab), the Electrons source width = 5 and the Electrons source weight = 0.005 (under Sources in the **Fluence** tab).

Perform auto-modeling with respect to Electron Contamination. The measured and computed depth dose curves should now match also before D_{max}. Use a high resolution when modeling electron contamination (0.2 cm is recommended).

It may be necessary to iteratively run the photon energy spectrum, electron contamination and output factor correction auto-modeling steps a couple of times to get a good match for the whole depth dose curve. Then turn to the profiles.

Step 6 – Beam Profile and Off Axis Softening

When the depth dose curves match, it is time to turn to the profiles. Open the Off Axis tab and start with the high dose region of the profiles. Look at the x, y and diagonal profiles of the largest field size. If necessary, add or remove radii points to the **Off-axis softening** and/or **Beam profile correction** tables.

If the measured curves look irregular, more radii points are needed while smooth measured curves need fewer points. It is often easier to get a better model with more radial points. It is especially important to have points defined near the penumbra for the largest measured field size. Values at radii larger than 95% of the maximum field size will not be affected by auto modeling and should be manually tuned. This corresponds to values at radii larger than 19 cm if the largest field size is 40 cm. Auto modeling will automatically insert a point to be modeled at a radius just smaller than this. If no diagonal profiles are imported for the largest field seize, use the Beam 3D module to correctly tune values for large radii affecting corner dose of the largest field size.

Perform auto-modeling with respect to **Off Axis Softening (Analytical)** and **Beam Profile Corrections (Analytical)**. Both Off-axis softening and Beam profile correction have to have points at the origin (radius 0.0 cm) and at "infinity" (recommended is 50.0 cm). For the Off-axis softening, the point at the origin must have value 0.0 cm and the value at infinity is usually between -20 cm and -30 cm. If the curves do not match sufficiently it might be useful to add more radial points, change the curves that are used in the auto-modeling step and/or use the steps **Off Axis Softening** or **Beam Profile Corrections** instead. Those steps use a gradient based optimization to model the parameters.

For the Beam profile correction, all factors should not deviate from 1.0 with more than approximately 10% in the in-field region for machines with flattening filter. If the beam profile correction factors show larger differences, review the beam model parameters. See typical values in *section 4.3.10 Summary of the beam model parameters on page 158*.

Some LINACs have a circular primary collimator close to the source which limits the field to a circular shape which is smaller than the diagonal of the largest square fields, such that the corners are cut off. To model this, start by setting the Beam Profile to zero (or close to zero) from the primary collimator radius and onwards. The exact shape shall be tuned to match diagonal measurements of the largest field size. If no diagonal profiles are imported into Beam Commissioning, the Beam Profile correction and the Off Axis Softening at radii larger than the largest profile can be validated and adjusted by comparing Beam 3D modeling doses to measurements in the corner. If so, manual tuning is necessary for values at large radii.

If there are differences between measured and computed curves at all depths, use beam profile correction. If the match is good at one depth but worse at other depths, use the Off axis softening.

After this step, the in-field dose region for the profiles should match at all depths.

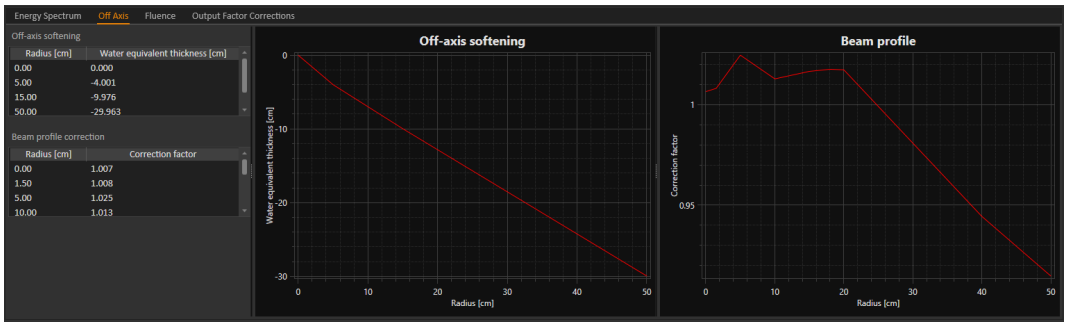


Figure 96. The Off axis tab.

Step 7 – Sources

Open the **Fluence** tab and turn to the penumbra region of the profiles. It is affected by the source weights and sizes, collimator calibration parameters and detector sizes.

If MLC collimated fields are used, the computed curves are also dependent on the MLC parameters and these should be tuned simultaneously. If jaw collimated fields are used, the jaw parameters should be tuned instead. Use the auto-modeling step **Collimator calibration (Analytical)** and manual tuning to do this. See step 8 for information on the collimator calibration.

First verify that the lateral detector width matches the size of the lateral dimension of the detector which was used to measure the curves (see *Detector sizes for photon curves on page 102* for a description of the detector resolution). If the detector width is large, the detector will yield measurements with a broader penumbra than the actual penumbra in the water phantom. If this is not modeled the broadened penumbra will falsely be assigned to spatially larger sources.

Perform auto-modeling with respect to **Primary Source** and **Flattening Filter Source**. The source widths can also be adjusted manually. Use the steepness of the penumbra region of dose profiles to determine these parameters. To get steeper calculated penumbra, decrease the width of the primary source in x or y direction, to get a broader penumbra, increase the primary source width. To get a good fit it is often necessary to have a high dose grid resolution during auto-modeling.

The **Flattening Filter** source width and weight can also be adjusted manually. Use the tails and shoulders of the x and y profiles. To get higher tails and more leaning shoulders increase the flattening filter width and/or weight. The flattening filter parameters give a variation with field size since the relative contribution of the scatter source inside the field edges increases with the field size.

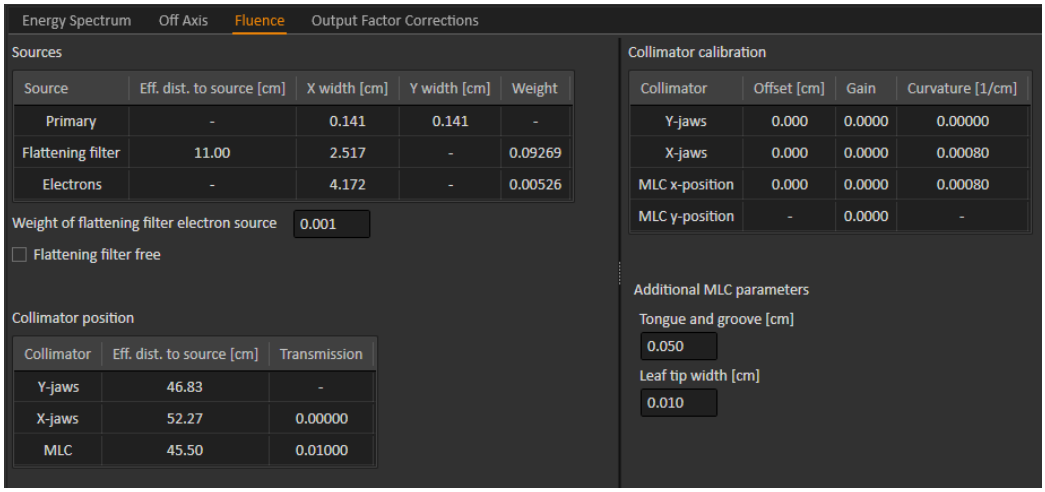

Energy Spectrum
Off Axis
Fluence
Output Factor Corrections
Sources
Source | Eff. dist. to source [cm] | X width [cm] | Y width [cm] | Weight
Primary | - | 0.141 | 0.141 | -
Flattening filter | 11.00 | 2.517 | - | 0.09269
Electrons | - | 4.172 | - | 0.00526
Weight of flattening filter electron source 0.001
Flattening filter free
Collimator position
Collimator | Eff. dist. to source [cm] | Transmission
Y-jaws | 46.83 | -
X-jaws | 52.27 | 0.00000
MLC | 45.50 | 0.01000
Collimator calibration
Collimator | Offset [cm] | Gain | Curvature [1/cm]
Y-jaws | 0.000 | 0.0000 | 0.00000
X-jaws | 0.000 | 0.0000 | 0.00080
MLC x-position | 0.000 | 0.0000 | 0.00080
MLC y-position | - | 0.0000 | -
Additional MLC parameters
Tongue and groove [cm]
0.050
Leaf tip width [cm]
0.010

Figure 97. The Fluence tab.

Step 8 – Collimator calibrations

The **Collimator calibration** parameters **Offset** and **Curvature** can be used to model the penumbra region of the profiles. Depending on the profile type (X or Y) and the collimation of the measured curves (only MLC or only jaws) the **Y-Jaws**, **X-Jaws** or **MLC position** can be adjusted. Look at approximately the FWHM point of the penumbra. If the measured curve is wider than the computed curve, apply a positive offset or curvature. If the computed curve is wider than the measured curve, apply a negative offset or curvature. If the mismatch between measured and computed curves is approximately the same for all field sizes, use the **Offset** parameter which offsets the computed curves equally independent of the position. If the mismatch only occurs for larger field sizes, use the **Curvature** parameter which offsets the computed curves more with increasing radius. See *Collimator calibration on page 144* for more information.

Step 9 – Off axis

The parameters in the **Off Axis** tab depend on the flattening filter and the source sizes and weights. Return to these parameters (step 6) and fine tune them if necessary after finishing the penumbra region modeling.

Step 10 – Depth dose curves revisited

Return to the depth dose curves (step 3 and step 4) and if necessary, perform auto-modeling with respect to **Energy Spectrum** and **Output Factor Corrections**.

Step 11 – MLC parameters

If MLC collimated fields are used, try to tune the MLC parameters **Tongue and groove**, **Leaf tip width** and **MLC Collimator calibration x-position** (y-position if MLC type Y). The MLC x-position (y-position if MLC type Y) **Offset** can be compared to a MLC leaf gap.

The MLC parameters are not always possible to model based only on the measured curves for rectangular fields, especially if they were measured with only jaws. Comparing 3D dose calculations from the main RayStation application or from the Beam 3D Modeling module with measurements

is the only way to correctly calibrate these parameters. These parameters are especially important to model correctly for machines to be used for SMLC, DMLC, VMAT and Conformal Arc treatments.

Step 12 – Verify and adjust the beam model using Beam 3D modeling

Use the Beam 3D modeling workspace to compute dose for field setups and regions that are clinically relevant but not possible to evaluate in the Beam Commissioning workspace. Beam 3D modeling can used for beam model tuning and to determine the limits of operation for your beam model, both for open and wedged fields. Test fields can be created in Beam 3D modeling directly or imported using DICOM.

One example is that dose can be computed for cases sensitive to MLC parameters such as e.g., sweeping gaps, picket fences, garden fences and generally differently sized, positioned and collimated fields.

Note: *This is just a set of examples of tests that can, and should be performed. Before commencing treatment with a new beam model, the user is expected to verify dose accuracy for all situations that may occur in the local clinical practice.*

Step-by-step instruction for commissioning of physical wedges

Make sure that the correct maximum field size is entered for your wedge. It is also important that you have measured curves up to the maximum allowed field size in order to evaluate your wedge model. Please note that any imperfection in the open model will affect the fit of the wedge curves. Certain characteristics of the beam model, like the exact field width (affected by the collimator calibration) or the electron contamination, are also not possible to modify with the wedge model.

Step 1 – Multi-parameter wedge modeling

Start modeling by running the step "Multi-parameter wedge auto modeling". This will optimize the material factor, wedge modulation parameters and wedge source parameters simultaneously. If the model needs more work, continue with step 2-6.

For standard wedges the transmission coordinates should be defined manually. Make sure to include coordinates at the edges and at any non-smooth point on the wedge. If you have corresponding measurements, it is also a good idea to add coordinates along the none-wedged axis, even though the wedge may be physically flat along that direction. It is generally a good idea to have as few coordinates as possible; too many coordinates may slow down the auto-modeling. Transmission values in the wedged direction can be initialized flat, to a value close to the central axis transmission. Correction values in the none-wedged direction can be initialized to 1.

Step 2 – Material factor

When the profiles for the largest field size look reasonable the Material factor should be adjusted so that the depth dose curves for the largest field size fit. A higher value will result in more beam hardening, i.e. a less inclined depth dose curve.

Note: *Dose curves for smaller field sizes may not match at this point.*

Step 3 – Wedge shape

Run an auto-modeling of the Wedge Shape for the largest field size. For Standard wedges, add or remove coordinates as needed.

Step 4 – Scatter source

The field size behavior is mainly affected by the scatter source. By changing the source weight, width and effective distance to the primary source, it is possible to obtain a better fit for smaller field sizes. Since the wedge is asymmetric and scatter is forward peeked, the scatter will also change the shape of the dose. Run an auto-modeling of the Wedge Scatter Source.

Step 5 - Return to the wedge shape

It might be necessary to modify the wedge shape, material factor and scatter source iteratively a few times before a good fit is reached. Identify the areas that need improvements and edit manually or do auto-modeling.

Step 6 - Wedge factor corrections

If there is a problem to obtain a good field size behavior, for example because of a bad fit in the buildup region, it might be necessary to use wedge factor corrections. Add a correction for each measured field size and edit them or run a Wedge Factor Correction auto-modeling.

It is also possible that the scatter source (which adds an asymmetric dose contribution) may affect the shape of the dose too much, e.g. if the tail region is too high or if it is difficult to match the shape for the smaller field sizes. In that case, reduce the scatter source weight, perform a corresponding change to the wedge shape and use the wedge factor corrections to catch the remaining field size behavior.

Note: *It is not possible to change the electron contamination source specifically for wedges. This means that the buildup region, especially for higher energies, may not fit the measured curves.*

Commission the machine

When satisfied with the beam model, commission the machine by right-clicking the machine name and selecting **Commission**. In order to verify that all beam model parameters are reasonable and that the fit between measured and computed curves is satisfactory before commissioning, a wizard is started that will guide the user through the review process. After the beam model has been reviewed, enter the user password in the Authentication dialog. Cancel the wizard at any time to review or correct items as needed.

4.8.7 Tips and tricks

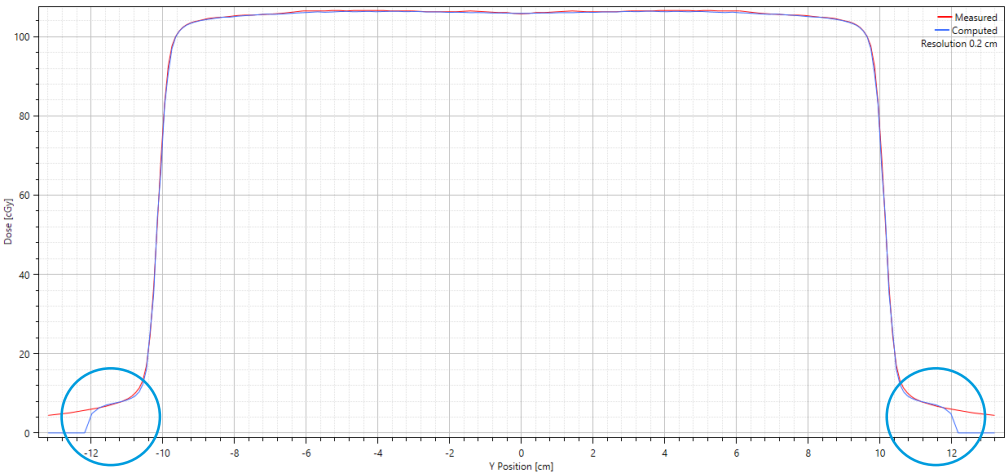
- The default target profiles for the in-field parameters is the largest existing field size; if the normalization of the profiles is not good (due to the poor fit of the depth dose curve), this could lead to problems at all depths. If this is the case, it is a good idea to use a smaller field size when performing auto-modeling of **Off Axis Softening** and **Beam Profile Corrections**.
- If the depth dose curves are not matching, it is appropriate to run additional iterations of the **photon energy spectrum and output factor corrections** script.
- Mismatch in the build-up region of the depth dose curves can most likely be fixed with the electron parameters. If the computed curves are over-shooting the measured ones, reduce the **Electrons Source** width and/or weight. Sometimes a couple of iterations with auto-modeling with respect to the **Electron Contamination** and the **Energy Spectrum and Output Factor Corrections** are needed to improve the build-up region.
- If the depth dose curves do not match, especially in the build-up region, go over the **Measurement conditions**; are **Depth offset** and **Detector height** correct?
- When auto-modeling with respect to **Energy Spectrum and Output Factor Corrections**, sometimes the smallest energy bin gets a very high value, especially if the electron contamination has been turned off. If this happens, turn on the electron contamination again or increase the weight of the Electrons Source. Manually adjust the smallest energy bin back to a reasonable value and redo the auto-modeling with respect to **Energy Spectrum and Output Factor Corrections**.
- If the profiles do not match, look at the parameters under the **Fluence** and **Off Axis** tabs. If the profiles match worse with larger depth, especially at larger radii, modify the **Off-axis softening**. If the profiles match equally bad for different depths, use the **Beam profile corrections** to improve the fit. More radial points may have to be added. If the penumbra regions do not match well, look at the position, widths and weights of the **Primary** and **Flattening filter Sources** under the **Fluence** tab.
- If the profiles do not match in the penumbra region, go over the **Measurement conditions**, is the **Detector width** correct, is **Field collimation** correct? A finer **Resolution** may be needed (0.2 cm is suitable when modeling the profiles).
- The **Collimator calibration** is used to account for the fact that the collimators are modeled as having zero thickness when they in reality are extended in the z direction. The effect of an MLC gap can also be modeled here. These effects are hard to fully model based only on rectangular field measurements. If the machine model is to be used for SMLC, DMLC and VMAT treatments where the MLC parameters are important, the **MLC Collimator calibration** parameters and the **Additional MLC parameters** should be tuned, by comparing calculated 3D dose in the main RayStation application or from the Beam 3D Modeling module with measurements.
- If the steepness of the penumbra does not fit well, first tune the source sizes before attempting to adjust the collimator calibration parameters. Note that source sizes usually have a larger impact on the smaller fields.

- If the curves begin to look strange, go over the parameter values as some of them might deviate from what is reasonable. Typical values for the different parameters are listed in table in *section 4.3.10 Summary of the beam model parameters on page 158*.
- The beam model is only valid for the field sizes present in the measured input data. Extrapolations can be made, but these are extremely sensitive to the output factor corrections set for these field sizes, and this has to be validated by other means than the measured curves in beam commissioning. The auto-modeling will not give reliable results for points not covered by the measured data.

4.8.8 Common problems and solutions

The following section illustrates a few common problems that may be encountered during beam commissioning, and how to solve them.

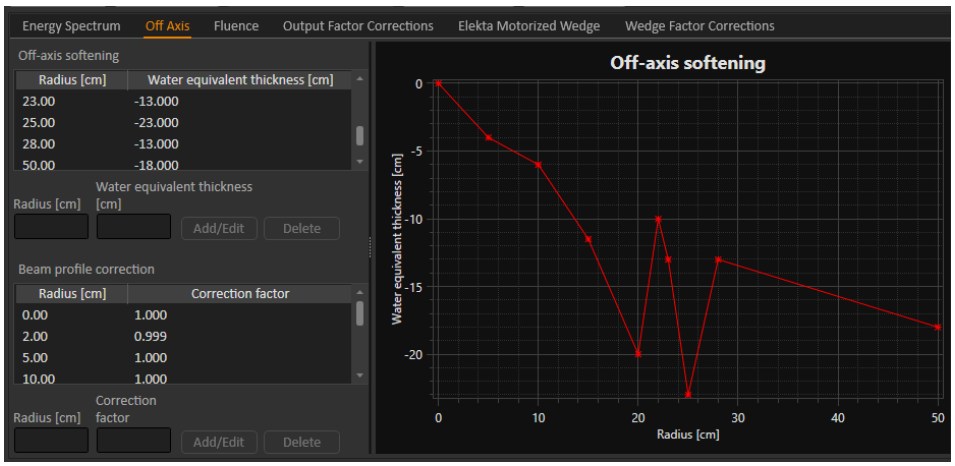
Problem 1: Sudden drop in dose at a certain radius from CAX.



Solution: Increase Phantom size in Measurement conditions. Note that this will also slightly increase scatter.

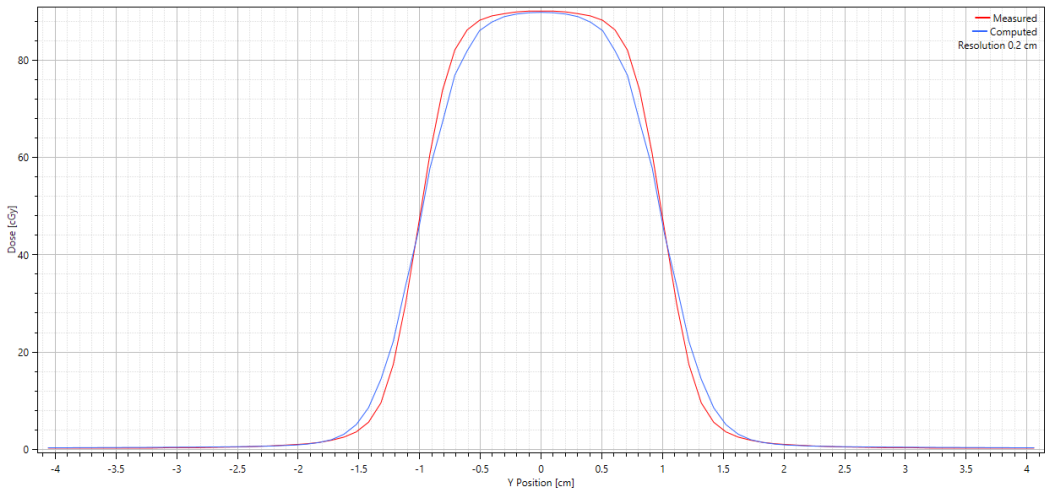
Problem 2: Jagged Off Axis Softening or Beam Profile Corrections curve.

This can sometimes be the result of running the auto-modeling scripts **Off Axis Softening** or **Beam Profile Corrections**.



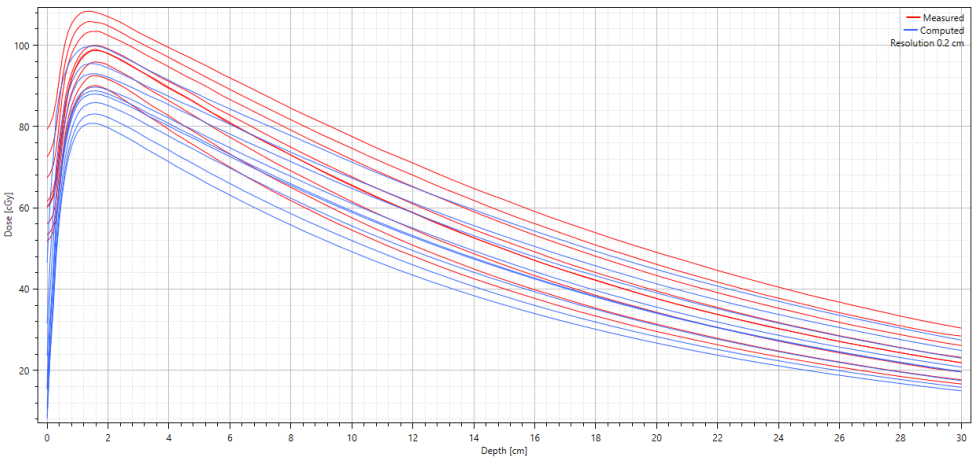
Solution: Manually change the points on the curve to something physically reasonable and/or run the scripts **Off Axis Softening (Analytical)** or **Beam Profile Corrections (Analytical)** instead.

Problem 3: Wrong penumbra steepness.



Solution: First verify that the detector width set in Measurement conditions is correct. If the problem persists, decrease primary source size in relevant direction (X or Y) for a narrower penumbra and increase source size for a broader penumbra.

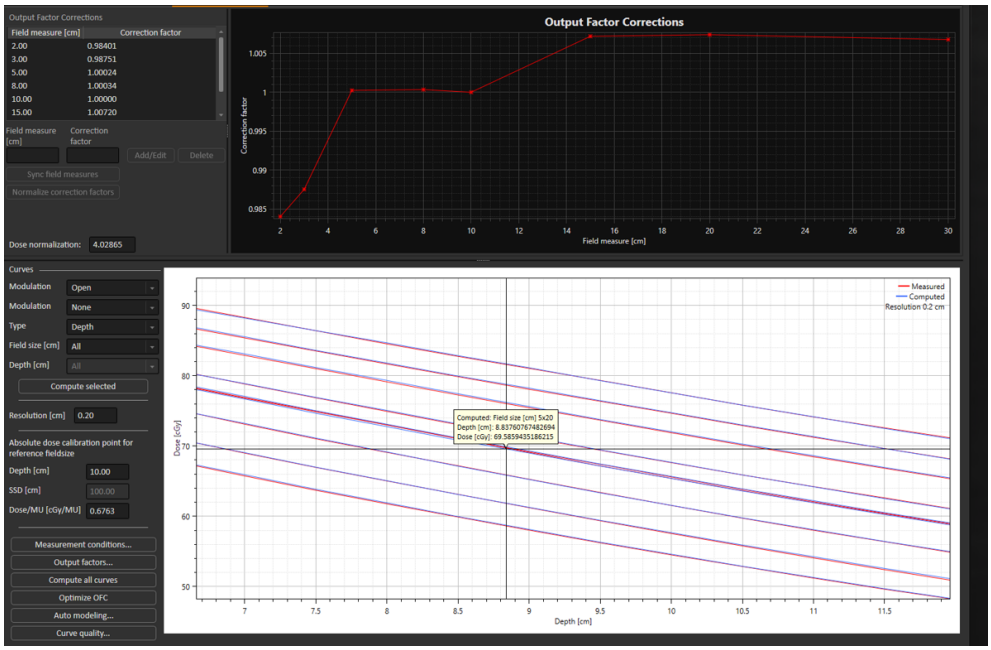
Problem 4: Normalization is incorrect.



Solution: Run the **Optimize OFC** script.

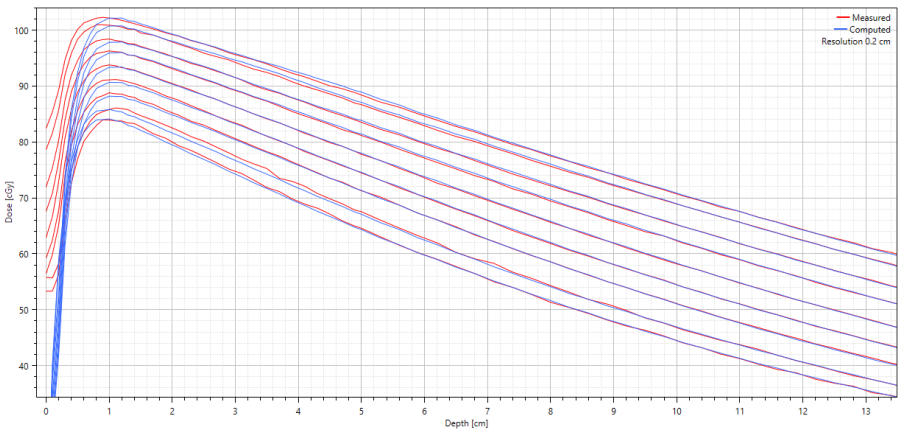
Problem 5: Problems with normalization for asymmetric fields.

For example: 5x20 cm^2 and 30x5 cm^2.



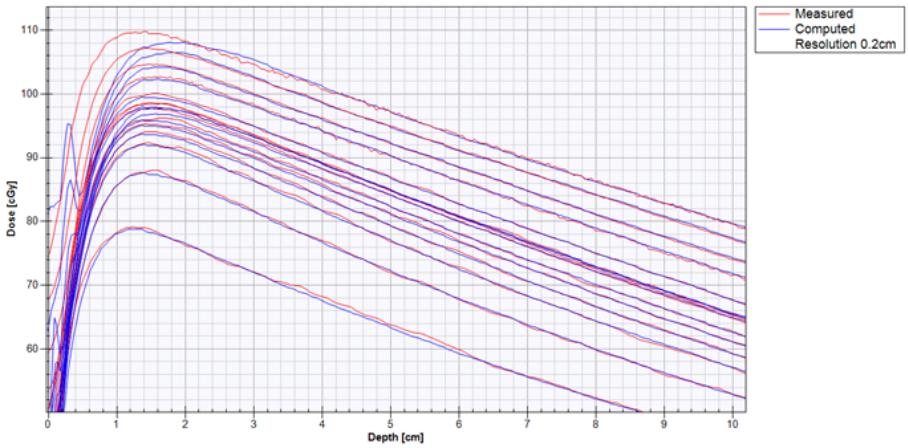
Solution: Add Output Factor Corrections for the asymmetric fields. Use the **Sync field measures** button to populate the output factor corrections list with one field measure per imported field size.Then run **Optimize OFC** again.

Problem 6: Missing dose in build-up for large fields.



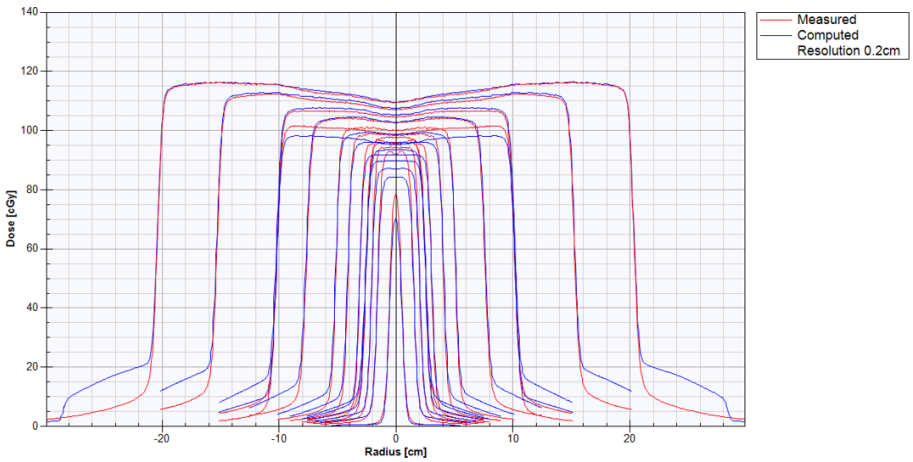
Solution: Decrease electron source width or increase weight. Possibly a combination.

Problem 7: Bump in build-up region.



Solution: Change the contamination electron energy spectrum by increasing E_0 or the width of the electron source.

Problem 8: Too high dose out-of-field.



Solution: Decrease weight of flattening filter source and run the **Optimize OFC** script.

4.9 HOW TO CREATE AN ELECTRON BEAM MODEL

This section gives advice on how to create an electron beam model.

In this section

This section contains the following sub-sections:

4.9.1	Resolution	p. 216
4.9.2	Number of histories	p. 217
4.9.3	Steps before electron beam modeling	p. 218
4.9.4	Fit the model parameters to the measured data	p. 220
4.9.5	Tips and tricks	p. 222

4.9.1 Resolution

For electron curves, resolution controls the size of the cubic voxels in the Monte Carlo simulation dose grid. A low resolution (≥ 0.4 cm) results in faster calculations and can be used in the beginning of modeling, but can make it difficult to model certain parts of the curves, e.g., profile shoulders. For air curves, the resolution parameter controls the size of the bixels over which the electron fluence is scored. In order to commission the machine, all electron curves must have been computed with a resolution of 0.2 cm or better.

4.9.2 Number of histories

Typically, about 100 000 histories per area fluence are needed to get a small enough statistical uncertainty in the water dose curves so that changes to the model can be evaluated. For intermediate steps, e.g., for the first normalization of the water profiles, a lower number of histories may be sufficient. Before commissioning, the dose curves have to be calculated using at least 250 000 histories for applicator curves and 25 000 histories for air profile curves.

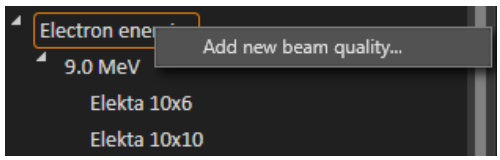
4.9.3 Steps before electron beam modeling

1. Right click on an existing treatment machine (Template, Commissioned, Uncommissioned or Deprecated) and select **Copy**. Choose a machine as similar as possible to the one you are about to commission regarding for example collimator properties.

   Note: *A machine needs to have at least one photon beam quality to be commissioned.*

2. Enter **Edit mode** for the copied machine.
3. Change the name of the machine in the **General** tab, optionally enter comments, and edit the static machine properties and optimization parameters described in *section 4.2 Machine properties on page 110*.
4. Make sure that the machine is Electron beam capable. This property is set in the **General** tab.
5. Fill in values for the scattering foil positions in the **Geometric** tab.
   - The **Primary scattering foil position** should be close to 0 cm. The value of this parameter is currently not used in the simulation.
   - The **Secondary scattering foil position** should be set to the location of the secondary scattering foil.
   - If the machine has a millstone collimator, select **The machine has millstone** checkbox and fill in the appropriate values.
6. Verify that the positions and thicknesses of the jaw(s) and MLC are correct. These parameters are used by the electron phase space engine.

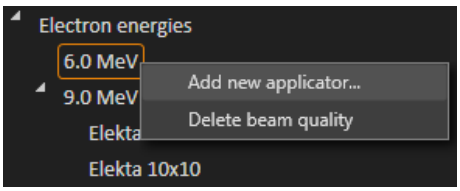
   For photon beam qualities, these parameters are only used if the machine lacks backup jaws so make sure to check these values even if you start out with a commissioned photon model.
7. Add the electron beam qualities supported by the machine:
   a. Right click on "Electron energies" in the machine tree view and select **Add new beam quality...**.

   b. Enter the **Nominal energy** in the **Add Beam Quality** dialog that opens and click **OK**.
   c. Repeat for all electron beam qualities.

8. Add applicators to the electron beam qualities:

   a. Right click on the electron beam quality and select **Add new applicator...**.



   b. Select applicator in the **Add applicator** dialog that opens and click **OK**.

      RayStation is installed with a number of template applicators which can be selected in the dialog. Review the properties of the applicator in the **Electron Applicator** tab and make adjustments if necessary. If an applicator of a specific vendor type has been added, the template applicator list in the **Add applicator** dialog will be filtered to only show applicators of the same type.

   c. Repeat for all applicators.

9. Set the correct SSD and absolute dose calibration point (depth and Dose/MU). The absolute dose calibration point on the beam quality level is applied to the open water depth dose curve (measured without applicator) and is only used to shift this curve relative to the applicator dose curves so that they can be compared. The absolute calibration point of the open depth dose curve does not affect the final beam model.

10. Import dose curves to the electron beam qualities and applicators. It is recommended to import all dose curves at this stage in order to quicker detect any measurement inconsistencies. For dose curve import, see section *section 4.1.2 Import curves on page 90*.

    Note: *The depth of the Absolute dose calibration point must be covered by the depth dose curve. If not, the message "All measured curves cannot be normalized" appears and no dose curves will be shown.*

4.9.4 Fit the model parameters to the measured data

Although there is a logical order in which to perform the modeling steps, the procedure is iterative, and it may be necessary to go back and redo a previous step to improve the model.

Model the electron energy spectrum

First make sure that the **Measurement depth** (under **Contamination photons**) is set to a proper value. The depth should be set to a point in the bremsstrahlung tail of the electron depth dose. The exact relative weight of the contamination photons is not so critical. Provide a reasonable guess. The electron energy spectrum parameters can be automodeled (**Optimize electron energy spectrum**) or set by hand. In general, the better the starting guess, the more likely it is that the optimization arrives at a good fit. The depth dose curves should match well, except for perhaps the first few mm. Points with a depth less than 2 mm are not considered in the fit. For a brief description of the spectrum parameters, see *section 4.4 Beam model parameters for electrons on page 161*.

Import the applicator dose curves if not already imported. Set the depth and dose per MU for the absolute dose calibration point for each applicator. Set the correct collimator positions under **Field shaping settings**.

Verify that the depth dose curves for the applicators are not too displaced compared to the open water depth dose curve. If that is the case, it may be helpful to enter a depth offset for the open curve (under **Measurement conditions**) to better match the applicator depth curves. If the depth offset is changed, the spectrum needs to be re-optimized.

Model the source phase space

Import the air profiles for the current energy if they have not already been imported. Use the profiles to adjust the source phase space parameters. The air profiles can be used to find a good first approximation of the phase space. Final adjustments and checks have to be done by comparing measured and calculated water profiles. To save time, work on one field size (using the curves filter and **Compute selected**) and periodically check the model using **Compute air profiles**. Keeping the number of histories low (below 10 000) and the resolution low (0.5 cm) will also speed up work. Start with the air profile for the largest field size.

When the air profiles have been adjusted, look at the applicator curves. Select an applicator and do **Compute dose curve contributions separately** for a relatively low number of histories (about 30 000). Normalize the computed curve to the measured curve using **Normalize computed**. Note that the contributions have to have been computed in order for the Normalize command to be available. Check the agreement for the depth dose curve. The curves should match fairly well. It is possible to **Scale dose contributions** to adjust the weight of the three contributions to the applicator dose curves: direct electrons, indirect electrons and photons.

When the normalization looks reasonable, recompute the curve using a larger number of histories. Look at a deep profile curve (at a depth where mostly contamination photons contribute to dose) for a large applicator to find the width of the contamination distribution. The applicator transmission factor also influences the shape of the deep profile curves. Possibly increase the resolution to 0.3 cm or finer. Look at the profiles for the largest applicator for the beam quality and fine-tune source phase space parameters.

When the model is almost complete, use **Compute all dose curves for the machine** to do an overnight calculation with for example 250 000 histories and use this to judge if modeling is complete.

4.9.5 Tips and tricks

When normalizing the air fluence profiles the average of all curves computed together is used as well as the average of the corresponding output factors. The normalized fluence for a certain field size will therefore be different if its profile is computed alone using **Compute selected** than if it is computed along with other field sizes using **Compute air profiles**.

The fluence cut-off radius should be mostly determined by the geometry of the primary collimator's opening cone angle and the position of the secondary scattering foil. A reasonable starting guess is about 3.5 cm.

If the penumbra of the air profile is too steep it may be because the angular spread is too small. Increasing the **Angular spread on axis parameter** and **Angular spread at cut-off radius** may help. If the computed profile does falls short of the shoulder of the measured profile, reduce the **Angular spread at cut-off radius**. Since the secondary scattering foil is thinner at the edges than in the center, the angular spread should decrease with radius. During modeling it may nevertheless be useful to try a constant angular spread first, when trying to match the ankle of the profile.

It will not be possible to model the tails (below 5% of fluence maximum) very accurately as the air fluence computation does not incorporate edge scatter from the collimators.

If a large profile curve has "horns", i.e., excess near the shoulder of the profile, try increasing the **Angular spread at cut-off radius** or narrowing the **Fluence distribution width**. The latter will typically also make the profile less flat at the center.

It is not always possible to get a perfect match between measured and computed air profiles. Even for a case where it is not possible to match the air fluence profiles to the measured curves, the applicator curves may still match well. The important thing is to get a good agreement for the applicator curves, since these correspond to the dose that will be calculated in patients in RayStation. The air profiles should be considered as a help to get a good starting guess for the source phase space parameters. It is worth computing the applicator curves now and then even if the air profiles do not match as well as expected.

If a computed applicator depth dose curve falls short of the measured curve in the region below dose maximum, try increasing the Indirect electron weight correction factor (under **Normalization** or in the **Scale dose contributions** dialog).

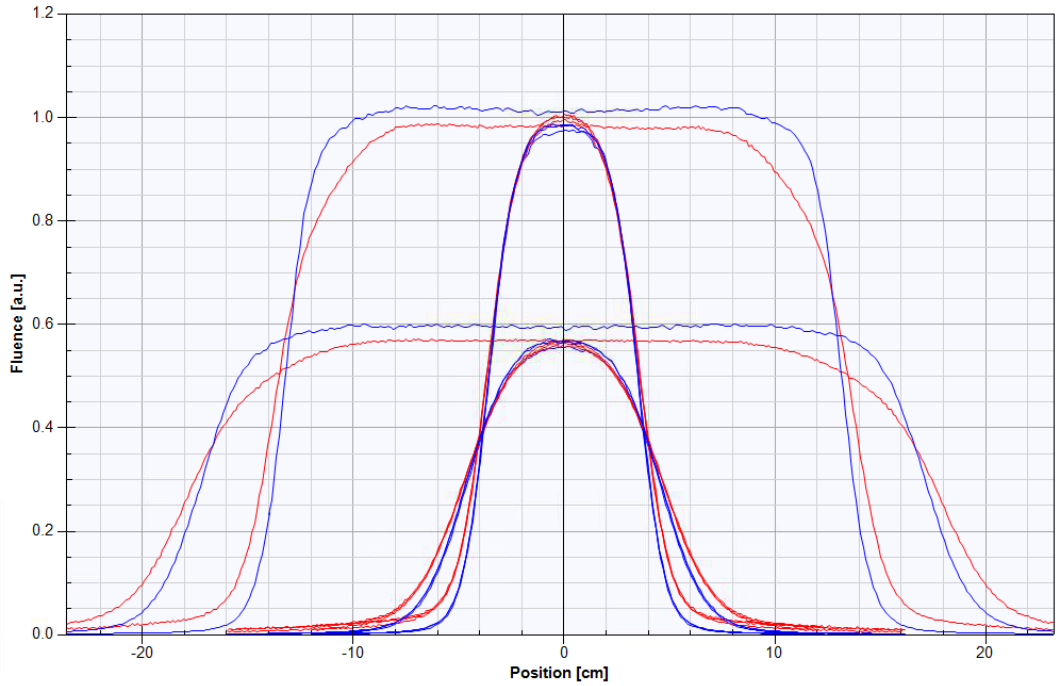


Figure 98. Sufficient match between measured and computed curves for air profiles.

5 TOMOTHERAPY LINAC TREATMENT MACHINES

This chapter describes the different machine and beam model parameters in the the Beam Commissioning module for TomoTherapy LINAC treatment machines. It also describes how to import Accuray beam model parameters, create a TomoTherapy machine model in RayPhysics, edit the machine properties, edit the beam model parameters and how to commission a machine.

In this chapter

This chapter contains the following sections:

5.1	Import Accuray beam model parameters	p. 226
5.2	Machine properties	p. 227
5.3	Beam model parameters	p. 235
5.4	Operations on dose curves	p. 242
5.5	How to create a TomoTherapy LINAC machine model	p. 246

5.1 IMPORT ACCURAY BEAM MODEL PARAMETERS

The first step in creating a TomoTherapy beam model is to import beam model parameters from the corresponding Accuray machine model.

Note: *It is necessary to start with an uncommissioned machine with the correct Accuray beam model, otherwise it will not be possible to finalize the import.*

To import Accuray beam model parameters:

1. Click the **Import from IDMS** button to open the **Import from IDMS** dialog.

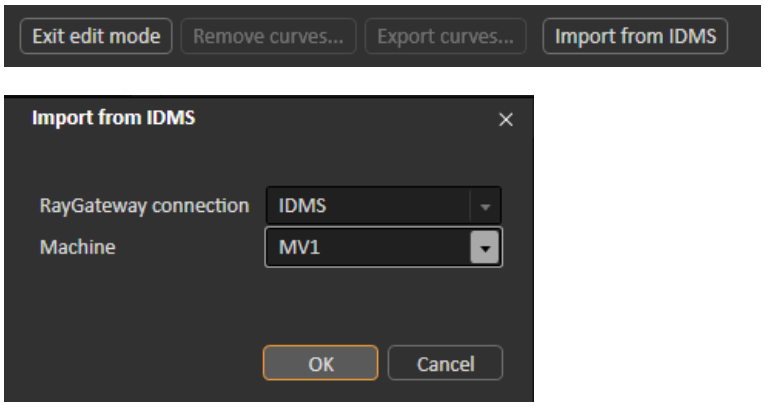


Figure 99. The **Import from IDMS** dialog where a RayGateway connection and a machine are selected.

The **RayGateway connection** drop-down list will show all RayGateway connections entered in the Clinic settings application and the **Machine** drop-down will show all machine models found in the selected IDMS.

2. Select a machine and click **OK**. This will start the import that will take a few minutes to finalize.

   When the import is finalized, all necessary beam model parameters from Accuray have been imported to the machine model.

5.2 MACHINE PROPERTIES

This chapter describes the machine properties which define the limits of what the machine can deliver. The parameters are shown in the right window when clicking on the machine name in the machine tree view. There are three tabs with different machine properties. Most machine constraints properties for TomoTherapy LINACs are not editable. The content of each tab is described in this chapter.

In this section

This section contains the following sub-sections:

5.2.1	General properties	p. 228
5.2.2	Jaws properties	p. 230
5.2.3	MLC properties	p. 232

5.2.1 General properties

This section describes the **General** tab in the machine constraints workspace.

Figure 100. The **General** tab.

Name

This is the name of the TomoTherapy LINAC which will be shown in RayStation. The name cannot be longer than 16 characters. The name of uncommissioned, template and commissioned machines must be unique.

Comment

This is a comment about the treatment machine visible to all users of the RayPhysics application.

IDMS machine ID

The machine ID that identifies the specific TomoTherapy machine in iDMS. Used in RayStation when exporting plans created with the machine model to send the plans to the correct TomoTherapy unit.

IDMS beam ID

The beam ID that identifies the specific TomoTherapy beam in iDMS. Used in RayStation when exporting plans created with the machine model to send the plans to the correct TomoTherapy unit.

IDMS machine revision

The version number of the machine in iDMS. Used in RayStation when exporting plans created with the machine model to verify that the machine model is up to date with the TomoTherapy unit.

IDMS beam revision

The version number of the beam in iDMS. Used in RayStation when exporting plans created with the machine model to verify that the machine model is up to date with the TomoTherapy unit.

SAD [cm]

The source axis distance (SAD) in cm.

Center of rotation offset [cm]

The center of rotation offset describes a shift in the MLC compared to the central axis of the machine. The center of rotation offset value is added to the MLC center positions in the MLC table to get the true position of the MLC leaves for a specific treatment machine. In RayStation, the center of rotation offset is used to offset the MLC leaf edges for target projections during optimization.

Bore size [cm]

The inner diameter of the bore of the gantry.

Number of projections per rotation

The number of projections, i.e., control points, that will be created during planning for each 360 degrees helical lap.

Minimum projection time [s]

The minimum possible duration for a projection, i.e., a control point.

Minimum couch speed [cm/s]

The minimum possible speed of the couch.

Maximum couch speed [cm/s]

The maximum possible speed of the couch.

Gantry rotation periods [s]

The **Gantry rotation periods** list contains the allowed discrete durations for one helical lap.

5.2.2 Jaws properties

This section describes the **Jaws** tab in the machine constraints workspace.

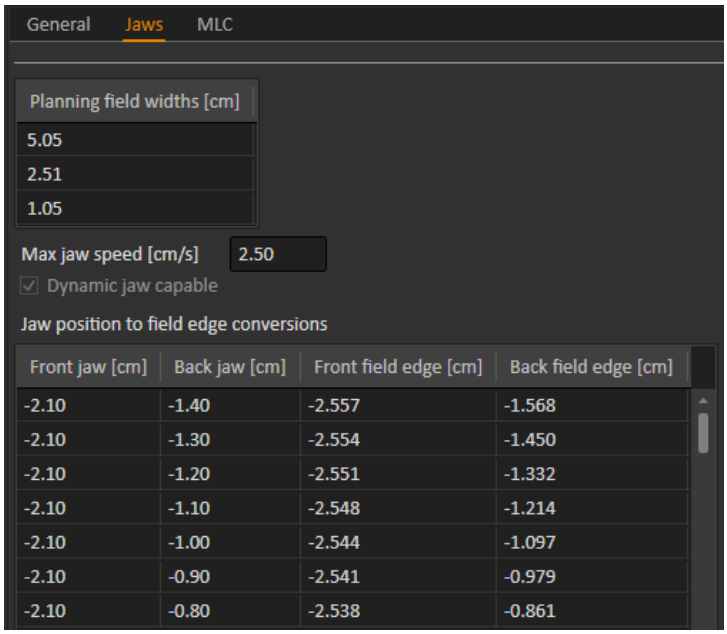


Figure 101. The **Jaws** tab.

Planning field widths [cm]

The different jaw field widths available for creating treatment plans. The field widths in the **Planning field widths** table are based on field edges (see *Jaw position to field edge conversions on page 230*).

Maximum jaw speed [cm/s]

The maximum jaw speed is used as a limit for jaw movement. This value is read from IDMS, but is editable by the user. It is possible to lower the maximum jaw speed to create less complex plans. Note that entering a higher value for the jaw speed than the one read from IDMS may result in plans that are not deliverable due to too high jaw speed.

Dynamic jaw capable

This option is checked if the machine is enabled for delivery of dynamic jaw plans.

Jaw position to field edge conversions

The position of the front and back jaw can be expressed in two different ways. One way is the machine instruction on how to position the jaw which is called jaw position and the other is the field edge which describes the location of the penumbra of a measured field at the isocenter. When the front or back jaw is at a specific position, the jaw position is always the same while the field edge of that jaw position also depends on the position of the other jaw. In RayStation, the jaw positions are saved to each segment in order to later be sent to the machine during delivery, but the field edges are

necessary information during plan optimization to get a correct target coverage and the field edges are also presented in the control point list and Beam's Eye View. To be able to convert between the jaw positions and field edges, a conversion table is stored in the machine model.

5.2.3 MLC properties

This section describes the **MLC** tab in the machine constraints workspace.

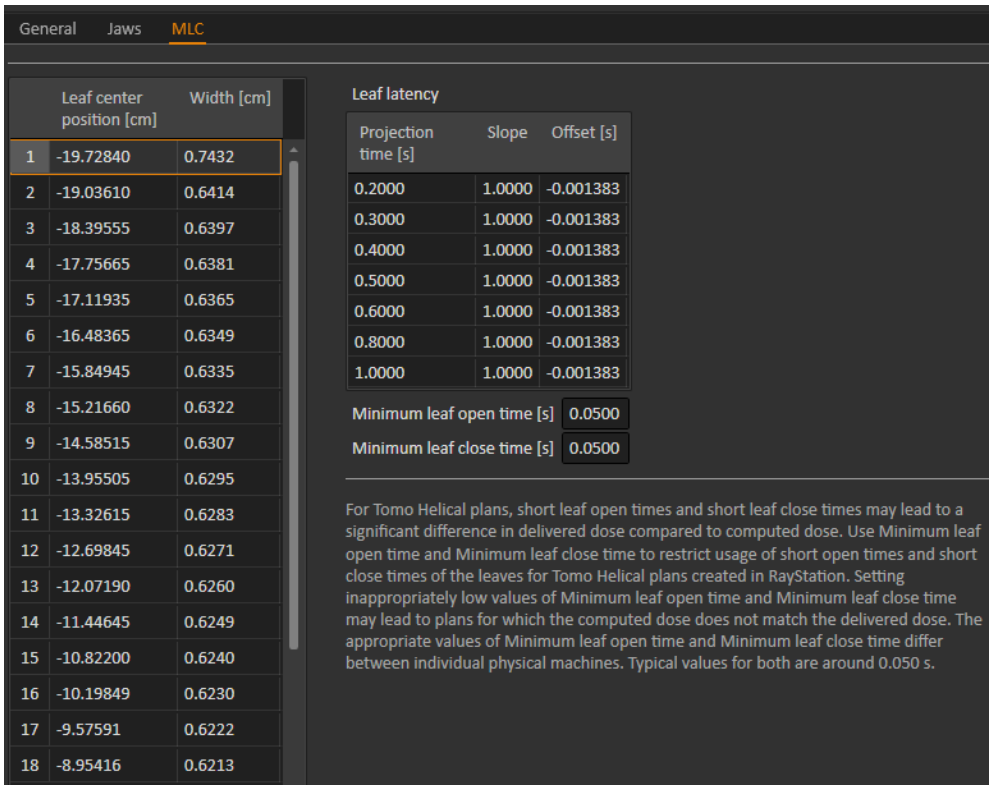

General
Jaws
MLC
Leaf center position [cm]
Width [cm]
1 -19.72840 0.7432
2 -19.03610 0.6414
3 -18.39555 0.6397
4 -17.75665 0.6381
5 -17.11935 0.6365
6 -16.48365 0.6349
7 -15.84945 0.6335
8 -15.21660 0.6322
9 -14.58515 0.6307
10 -13.95505 0.6295
11 -13.32615 0.6283
12 -12.69845 0.6271
13 -12.07190 0.6260
14 -11.44645 0.6249
15 -10.82200 0.6240
16 -10.19849 0.6230
17 -9.57591 0.6222
18 -8.95416 0.6213
Leaf latency
Projection time [s]
Slope
Offset [s]
0.2000 1.0000 -0.001383
0.3000 1.0000 -0.001383
0.4000 1.0000 -0.001383
0.5000 1.0000 -0.001383
0.6000 1.0000 -0.001383
0.8000 1.0000 -0.001383
1.0000 1.0000 -0.001383
Minimum leaf open time [s] 0.0500
Minimum leaf close time [s] 0.0500
For Tomo Helical plans, short leaf open times and short leaf close times may lead to a significant difference in delivered dose compared to computed dose. Use Minimum leaf open time and Minimum leaf close time to restrict usage of short open times and short close times of the leaves for Tomo Helical plans created in RayStation. Setting inappropriately low values of Minimum leaf open time and Minimum leaf close time may lead to plans for which the computed dose does not match the delivered dose. The appropriate values of Minimum leaf open time and Minimum leaf close time differ between individual physical machines. Typical values for both are around 0.050 s.

Figure 102. The **MLC** tab.

Leaf center position and width

The **MLC** table to the left in the **MLC** tab lists the leaves and their position and width. The **Leaf center position** [cm] entry describes the center position of the leaves along the x-axis of the IEC 61217 beam limiting device coordinate system. The **Width** [cm] entry describes the width of the individual MLC leaf in question, along the same axis as the center positions.

Leaf latency

The leaf latency consists of a table with **Slope** and **Offset** for different **Projection times**. Ideally, an MLC leaf would open or close instantaneously. In reality, there is a difference between the ideal, requested, leaf open time and the real, delivered, leaf open time for different projection times.

The relationship between requested time and delivered time is:

Delivered time = Slope × Requested time + Offset

When leaves have a short open time or a short close time, the leaf latency correction relationship is no longer valid which leads to differences between computed and delivered dose.

See *Minimum leaf open time [s] on page 233* and *Minimum leaf close time [s] on page 233* for information about how to avoid these leaf open times.

WARNING!

TomoTherapy leaf latency offsets affect both dose output and shape. Leaf latency offsets are imported from iDMS, and can also be edited in RayPhysics. Changes to leaf latency offsets may have different effect for different jaw field sizes, projection times and leaf opening times. Ensure that dose accuracy is validated for all jaw openings and over the full range of clinically relevant projection times and leaf opening times before using the model clinically. (530101)

Minimum leaf open time [s]

The minimum time a MLC leaf can be open during one projection. The minimum leaf open time is not read from IDMS but should be set to a value high enough to avoid leaf open times where the leaf latency correction is not correct. The appropriate value depends on the treatment machine. A typical value is 0.050 s. Setting the Minimum leaf open time to an inappropriately large value may lead to inferior plan quality.

Minimum leaf close time [s]

The minimum time a MLC leaf can be closed between two projections. A close time of zero, i.e. no closing at all, is always allowed regardless of the value of the minimum leaf close time. The minimum leaf close time is not read from IDMS but should be set to a value high enough to avoid leaf close times where the leaf latency correction is not correct. The appropriate value depends on the treatment machine. A typical value is 0.050 s. Setting the Minimum leaf close time to an inappropriately large value may lead to inferior plan quality.

WARNING!

TomoTherapy dose computation accuracy for short leaf open times and short leaf close times. For TomoHelical and TomoDirect plans with a large number of short leaf open times or a large number of short leaf close times, the delivered dose may differ significantly from the computed dose. The reason is that for fast leaf movements, the treatment machine will not open/close the leaves in accordance with the model used in the dose computation.

To avoid short leaf open times and short leaf close times when creating plans in RayStation, use the beam model parameters *Minimum leaf open time* and *Minimum leaf close time*. The issue will occur with certain machine specific leaf open/close time characteristics, but around 50 ms can normally be an appropriate value for both *Minimum leaf open time* and *Minimum leaf close time*.

To find the appropriate values for *Minimum leaf open time* and *Minimum leaf close time* for each TomoTherapy treatment unit, leaf latency data can be measured as described in *Westerly DC, Soisson E, Chen Q, Woch K, Schubert L, Olivera G and Mackie TR, Treatment planning to improve delivery accuracy and patient throughput in helical tomotherapy, Int J Radiat Oncol Biol Phys. 2009;74(4):1290–1297*. Another option is to use scripting to create a set of test plans with a constant leaf open time for all open leaves and then examine the relation between measured dose and opening time. (361442)

5.3 BEAM MODEL PARAMETERS

This chapter describes the beam model parameters for TomoTherapy LINACs.

In this section

This section contains the following sub-sections:

5.3.1	Energy Spectrum	p. 236
5.3.2	Transverse Profile	p. 238
5.3.3	MLC	p. 239
5.3.4	Jaws	p. 241

Precaution

WARNING!

TomoTherapy machine commissioning. When commissioning a TomoTherapy machine, most parameters are read from IDMS and only minor changes are expected to be required in the machine model in RayPhysics. The transverse profile, jaw fluence output factors and leaf latency offsets are overwritten in this process and may need to be updated.

Note that for TomoTherapy machines the computed dose curves in the Beam Commissioning module are normalized against the measured curves, i.e., the measured and computed dose curves will match in output regardless of the output of the beam model. The output of the model must therefore be adjusted and verified for all field widths using TomoHelical beams. For more information, refer to the *RSL-D-RS-9A-BCDS, RayStation 9A Beam Commissioning Data Specification*.

Note also that the MLC filters are not part of the dose curve calculation in the Beam Commissioning module in RayPhysics and their usage can only be verified using TomoHelical or TomoDirect beams.

The dose calculation must be validated for the relevant range of clinical treatment fields before clinical use. In addition to what is listed in warning 508815, validation shall include different jaw sizes and modes, projection times, opening fractions and pitches. (252208)

5.3.1 Energy Spectrum

This section describes the **Energy Spectrum** tab in the beam model workspace.

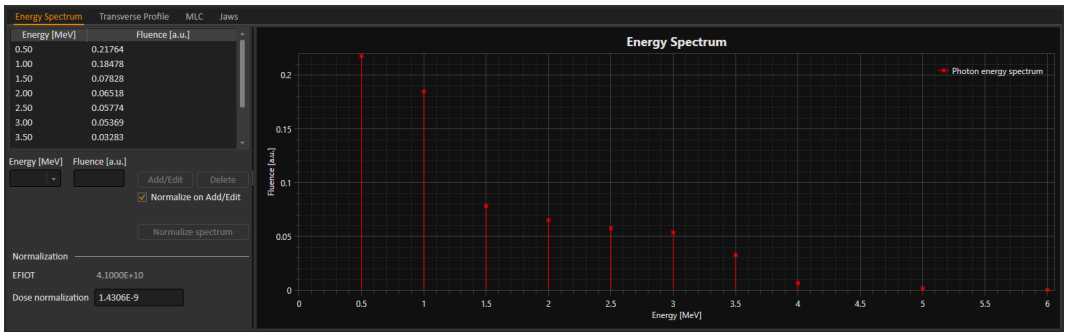


Figure 103. The **Energy Spectrum** tab.

Photon energy spectrum

The photon energy spectrum is entered as a list of mono-energetic contributions which combine to give a poly-energetic spectrum used in dose computation. All energy bins are smaller than or equal to the energy of the machine model, i.e., with energy bins up to 6 MeV for a beam quality with energy 6 MV. The spectrum can be normalized such that the energy fluence is 1 MeV by clicking the **Normalize spectrum** button. This changes the overall normalization of the beam model which can be corrected for by editing the **Dose normalization** value (described below).

To change the energy spectrum parameters, select the **Energy** (MeV) to be adjusted from the **Energy** list and enter the new **Fluence** (a.u.) in the **Fluence** list. The spectrum will be normalized automatically if the **Normalize on Add/Edit** checkbox is checked. The spectrum can also be normalized manually once all the values are edited by clicking the **Normalize spectrum** button.

A spectrum bar in RayPhysics 9A specifies integrated particle fluence weights at the energy of the bar. When comparing to an analytical shape, the weight is obtained by integrating over an energy range starting/ending halfway between the neighboring bars. For most points this results in symmetrical and equidistant intervals. At some energies there is a jump to a coarser grid resulting in a spectrum shape which looks unphysically skewed as the high energy bins are integrated over a larger energy interval.

EFIOT

EFIOT, Energy Fluence per Ideal Open Time, is the fluence output for the widest jaw opening in the Accuray model. A higher EFIOT means a higher dose rate for the machine. The computed fluence is scaled with the EFIOT value.

Dose normalization

The dose normalization is used to get the correct absolute output for the calculated dose. The dose normalization scales the fluence in all dose computations with the given beam model. Note that an overall normalization also can be hidden in the energy spectrum (when not normalized). The resulting

beam model is independent of how the normalization is performed. The dose normalization is editable by the user.

5.3.2 Transverse Profile

This section describes the **Transverse Profile** tab in the beam model workspace.

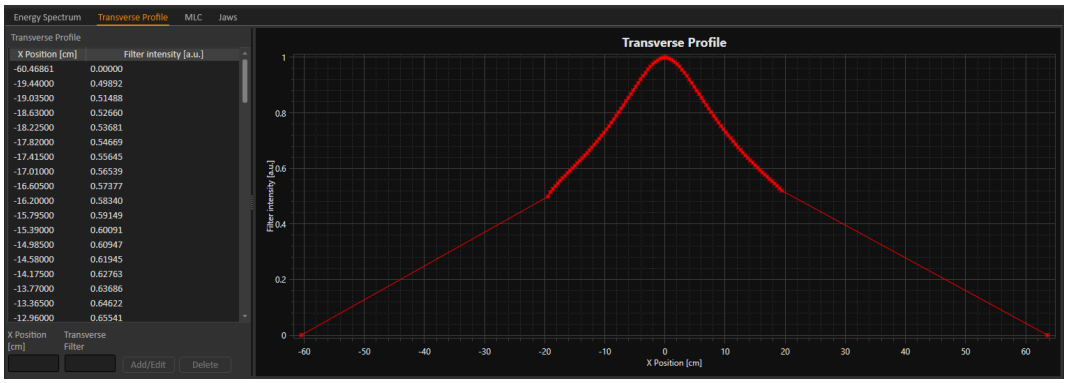


Figure 104. The **Transverse Profile** tab.

The fluence is scaled with a beam profile correction, the Transverse Profile, to account for the cone shape of the flattening filter free TomoTherapy beam.

The following operations can be performed in the **Transverse Profile** list:

- **Delete an entry.** Select it in the table and click **Delete**.
- **Add a new entry.** Enter the **X Position** and **Transverse Filter** intensity in the fields below the table and click **Add/Edit**.
- **Change the filter intensity at a point at a given X position.**

  1. Select the row that should be edited in the table.
  2. Enter the **X Position** and **Transverse Filter** intensity in the fields below the table and click **Add/Edit**.

     Note that marking a row, changing the X position and clicking **Add/Edit** creates a new entry and does not delete the originally selected value.

5.3.3 MLC

This section describes the **MLC** tab in the beam model workspace.

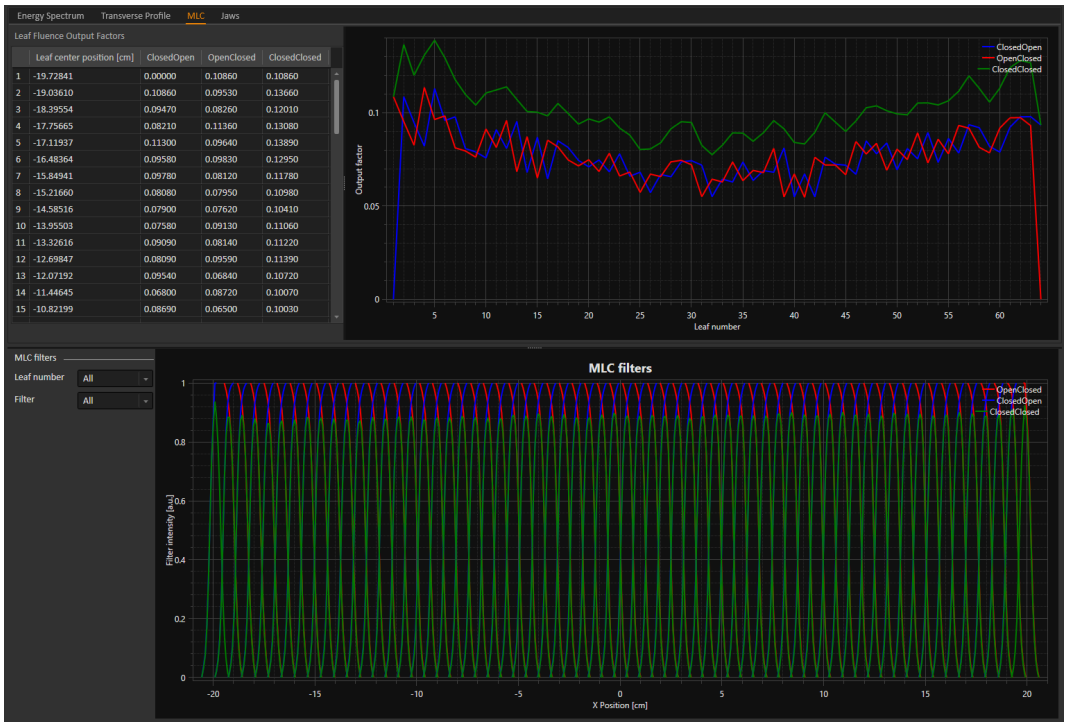


Figure 105. The **MLC** tab.

Leaf Fluence Output Factors

The Leaf Fluence Output Factors describe the decrease in integral fluence through MLC leaves depending on if the neighboring leaves are open or closed. The Leaf Fluence Output Factors can be used to update a treatment plan when changing between different machines to keep an ideal fluence. The Leaf Fluence Output Factors are not used by RayStation.

MLC filters

The MLC filters describe the penumbra effect of an MLC leaf edge. There are different filters depending on if the neighboring leaves are open or closed. There are three different types of filters:

- **OpenClosed** - The filter when the leafs left neighbor is open, the leaf is open, and the leafs right neighbor is closed.
- **ClosedOpen** - The filter when the leafs left neighbor is closed, the leaf is open, and the leafs right neighbor is open.
- **ClosedClosed** - The filter when the leafs left neighbor is closed, the leaf is open, and the leafs right neighbor is closed.

Each MLC leaf has one filter of each type. The exception is the first MLC leaf which does not have an OpenClosed filter and the last leaf which does not have a ClosedOpen filter.

Use the **Leaf number** and **Filter** drop-down lists to view different filters.

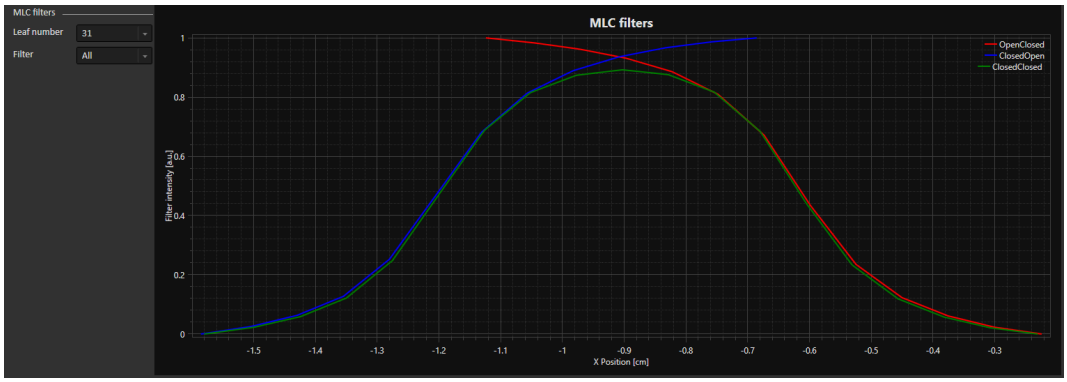


Figure 106. The illustration shows all three MLC filters for one MLC leaf.

5.3.4 Jaws

This section describes the **Jaws** tab in the beam model workspace.

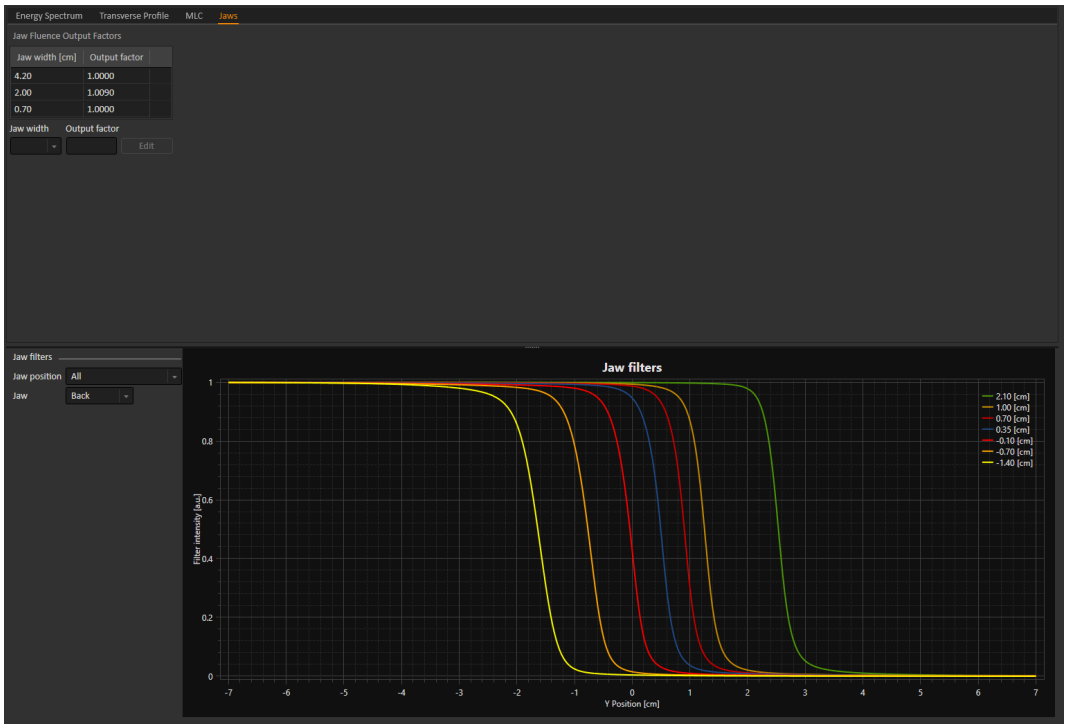


Figure 107. The **Jaws** tab.

Jaw Fluence Output Factors

The Jaw Fluence Output Factors are relative output factors applied to the fluence to correct for output differences between different jaw field widths. The **Jaw Fluence Output Factors** table lists output factors for different jaw widths. The jaw widths in the **Jaw Fluence Output Factors** table are based on jaw positions (see *Jaw position to field edge conversions on page 230*)

It is not possible to add or delete jaw widths but it is possible to edit the output factors. To change the output factor for a jaw width:

1. Select the row in the table or in the **Jaw width** drop-down list below the table.
2. Edit the **Output factor** in the field below the table, then click **Edit**.

Jaw filters

The jaw filters describe the jaw penumbra effect. There are different jaw filters for the front and back jaws at different jaw positions.

Use the **Jaw position** and **Jaw** drop-down lists to view different jaw filter combinations.

5.4 OPERATIONS ON DOSE CURVES

This chapter describes the operations that can be performed on dose curves for TomoTherapy LINACs.

In the **Energy Spectrum** and **Transverse Profile** tabs, the lower window shows measured and computed dose curves. TomoTherapy beam models are provided with a set of golden data measured dose curves. Normally, all TomoTherapy treatment units are tuned to closely match the golden data. The computed dose curves should be interpreted as showing relative dose, they are always normalized individually against the measured curves.

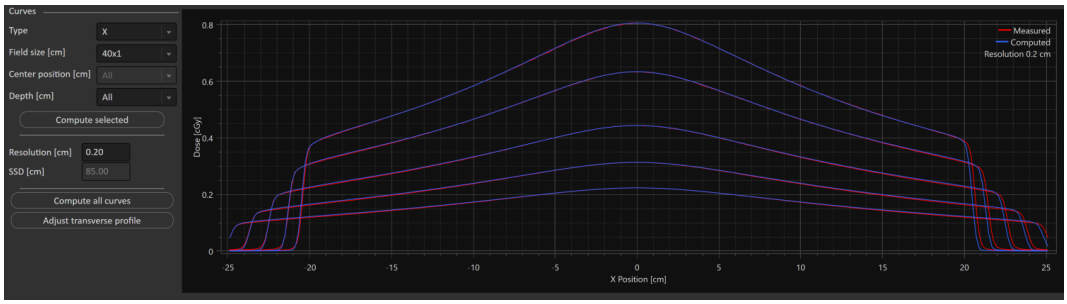


Figure 108. The dose curve window for TomoTherapy LINAC machines.

The following operations are possible to perform on the dose curves:

Compute selected – Compute dose curves for the measured curves that are visualized in the dose curve graph. This option also computes all other curves types with the same field size and center position as the visualized curves.

Compute all curves – Compute dose curves for all measured curves of the beam quality.

Adjust transverse profile - Modifies the filter intensities of the Transverse Profile to get the measured and computed curves to match better.

$$Transverse\ profile_{after\ adjustment}(r) = Transverse\ profile_{before\ adjustment}(r) \cdot \frac{1}{n_{curves}} \cdot \sum_{depths, field\ sizes} \frac{measured\ x{-}profile(x)}{computed\ x{-}profile(x)} \quad \text{[Eq. 18]}$$

Delete curves - Deletes the selected curves. For instructions, see *section 5.4.1 Delete curves on page 244*.

Export curves - Exports all measured and computed curves for a selected beam quality. For instructions, see *section 5.4.2 Export curves on page 245*.

In this section

This section contains the following sub-sections:

5.4.1	Delete curves	p. 244
5.4.2	Export curves	p. 245

5.4.1 Delete curves

TomoTherapy beam models are provided with a set of golden data dose curves. Normally, all of these dose curves shall be kept in the beam model. If the machine to be modeled is not dynamic jaw capable, it may be necessary to remove non-central Y-profiles.

If a depth dose curve is removed, all profiles of the same field size will be removed with it.

To delete a curve:

1. Click the **Remove curves** button to open the **Remove curves** dialog.

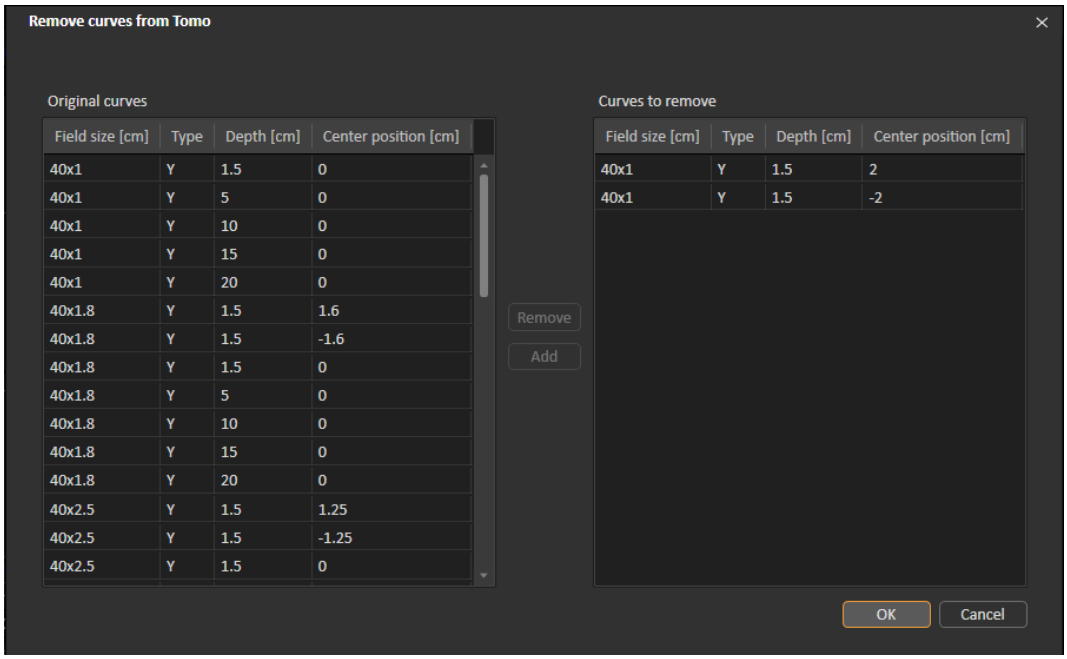


Figure 109. The **Remove curves** dialog.

2. Select a curve in the list and click the **Remove** button.
3. Click **OK**.

5.4.2 Export curves

All measured and computed curves for a selected beam quality can be exported to the csv format. Measured and computed curves (if available) are exported into separate files.

To export all curves for a selected beam quality:

1. Click the **Export curves** button.

   This opens the **Export dose curves** dialog showing all dose curves that are possible to export.

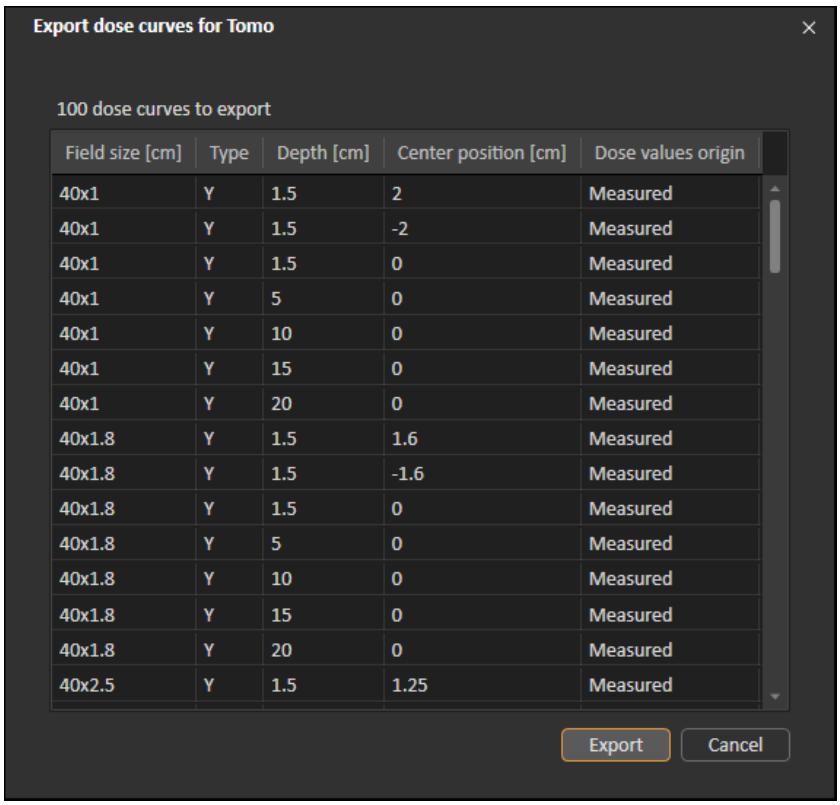

Export dose curves for Tomo
100 dose curves to export
Field size [cm] Type Depth [cm] Center position [cm] Dose values origin
40x1 Y 1.5 2 Measured
40x1 Y 1.5 -2 Measured
40x1 Y 1.5 0 Measured
40x1 Y 5 0 Measured
40x1 Y 10 0 Measured
40x1 Y 15 0 Measured
40x1 Y 20 0 Measured
40x1.8 Y 1.5 1.6 Measured
40x1.8 Y 1.5 -1.6 Measured
40x1.8 Y 1.5 0 Measured
40x1.8 Y 5 0 Measured
40x1.8 Y 10 0 Measured
40x1.8 Y 15 0 Measured
40x1.8 Y 20 0 Measured
40x2.5 Y 1.5 1.25 Measured
Export
Cancel

Figure 110. The **Export dose curves** dialog.

2. Select **Export** to export the curves.
3. In the browse dialog that opens, specify a location for the exported dose curves and click **OK**.

5.5 HOW TO CREATE A TOMOTHERAPY LINAC MACHINE MODEL

To create a TomoTherapy LINAC machine model in RayPhysics:

1. Start with a copy of the provided template machine.
2. Enter edit mode.
3. Import the beam model parameters from IDMS. (For instructions, see *section 5.1 Import Accuray beam model parameters on page 226*.)
4. Review the imported parameters.
5. Compute dose curves. The computed dose curves are normalized against the measured curves.
6. Check the match of the computed X profiles.

   Note that the measured dose curves are the golden data and may not correspond exactly to a specific TomoTherapy treatment unit.
7. If desired, manually edit the Transverse profile or run the Adjust transverse profile to get a better match to measured profiles. The transverse profile in the template is overwritten on import from IDMS.
8. Compute dose curves.
9. Check the output and update Dose normalization and Jaw fluence output factors as described in *RSL-D-RS-9A-BCDS, RayStation 9A Beam Commissioning Data Specification*.
10. Commission the machine by right-clicking the machine name and selecting **Commission**. In order to verify that all beam model parameters are reasonable and that the fit between measured and computed curves is satisfactory before commissioning, a wizard is started that will guide the user through the review process. After the beam model has been reviewed, enter the user password in the **Authentication** dialog. Cancel the wizard at any time to review or correct items as needed.

6 ION TREATMENT MACHINES

This chapter describes the functionality in the Beam Commissioning module for Ion treatment machines.

In RayPhysics it is possible to view and edit most of the machine parameters for machines in the machine database. For proton PBS and Line scanning machines, the full commissioning workflow is supported, including import and export of measurements, auto-modeling of the machine, dose computation and final commissioning. For carbon ion PBS, Hyperscan PBS and US/DS/Wobbling machines, a limited part of this functionality is available.

Modeling and final commissioning of carbon PBS, proton Hyperscan PBS and proton US/DS/Wobbling machines can only be performed by RaySearch staff. The uncommissioned machine together with the beam data measurements and with all visible and editable machine parameters reviewed and updated should be saved as an rsbak-file and sent to support@raysearchlabs.com for final commissioning.

In this chapter

This chapter contains the following sections:

6.1	Machine properties	p. 248
6.2	Beam quality parameters for Ion treatment machines	p. 274
6.3	Checklist before commissioning a proton PBS or Line scanning machine	p. 306

6.1 MACHINE PROPERTIES

This section describes the machine properties for Ion treatment machines. The parameters are shown in the right window when clicking the machine name in the machine tree view. The content of each tab is described in this section.

In this section

This section contains the following sub-sections:

6.1.1	General properties	p. 249
6.1.2	Beam line objects	p. 254
6.1.3	Setup imaging devices	p. 271
6.1.4	DICOM	p. 273

6.1.1 General properties

This section describes the **General** tab in the Machine properties workspace for Ion treatment machines.

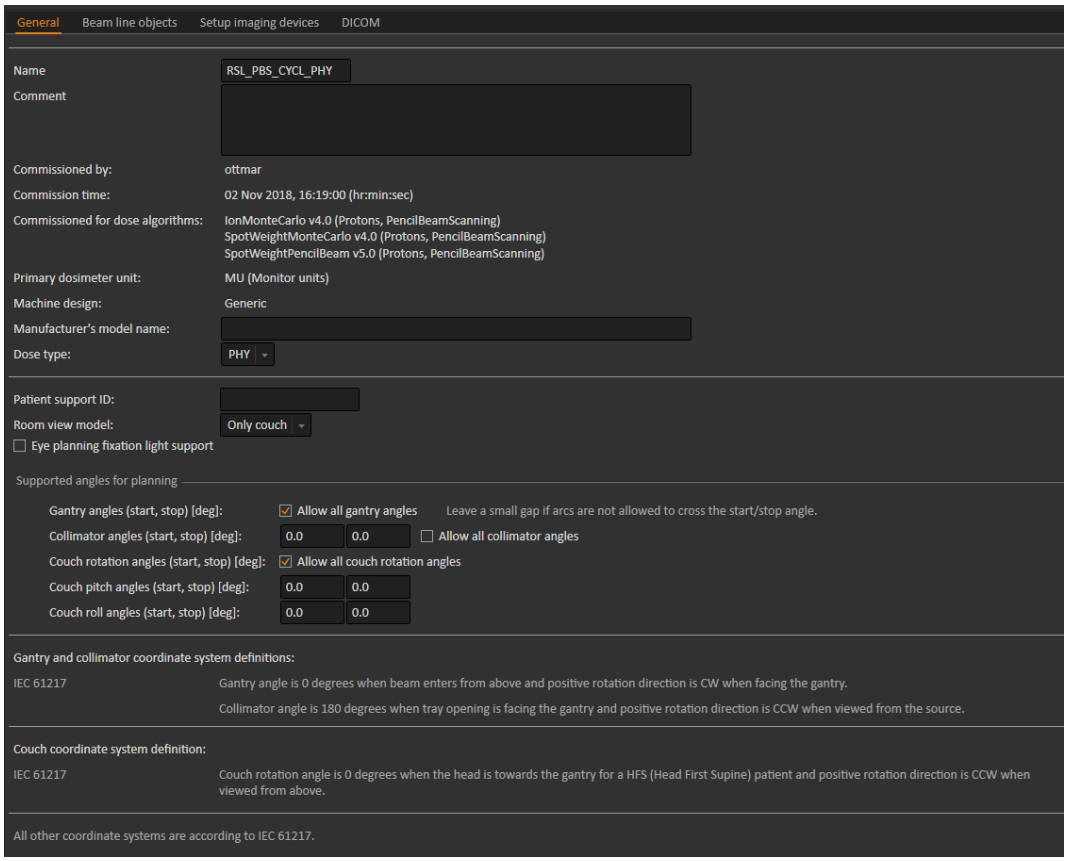

General
Beam line objects
Setup imaging devices
DICOM
Name
RSL_PBS_CYCL_PHY
Comment
Commissioned by:
ottmar
Commission time:
02 Nov 2018, 16:19:00 (hr:min:sec)
Commissioned for dose algorithms:
IonMonteCarlo v4.0 (Protons, PencilBeamScanning)
SpotWeightMonteCarlo v4.0 (Protons, PencilBeamScanning)
SpotWeightPencilBeam v5.0 (Protons, PencilBeamScanning)
Primary dosimeter unit:
MU (Monitor units)
Machine design:
Generic
Manufacturer's model name:
Dose type:
PHY
Patient support ID:
Room view model:
Only couch
Eye planning fixation light support
Supported angles for planning
Gantry angles (start, stop) [deg]:
Allow all gantry angles
Leave a small gap if arcs are not allowed to cross the start/stop angle.
Collimator angles (start, stop) [deg]:
0.0
0.0
Allow all collimator angles
Couch rotation angles (start, stop) [deg]:
Allow all couch rotation angles
Couch pitch angles (start, stop) [deg]:
0.0
0.0
Couch roll angles (start, stop) [deg]:
0.0
0.0
Gantry and collimator coordinate system definitions:
IEC 61217
Gantry angle is 0 degrees when beam enters from above and positive rotation direction is CW when facing the gantry.
Collimator angle is 180 degrees when tray opening is facing the gantry and positive rotation direction is CCW when viewed from the source.
Couch coordinate system definition:
IEC 61217
Couch rotation angle is 0 degrees when the head is towards the gantry for a HFS (Head First Supine) patient and positive rotation direction is CCW when viewed from above.
All other coordinate systems are according to IEC 61217.

Figure 111. The **General** tab in the Machine properties workspace.

Name

This is the name of the treatment machine which will be shown in the GUI and exported to DICOM. The name cannot be longer than 16 characters. The name of uncommissioned, template and commissioned machines must be unique.

Comment

This is a comment about the treatment machine visible to all users of the RayPhysics application.

Saved by / Saved time

These properties will be shown for uncommissioned machines and indicate the last time the machine was saved and by which user.

Dose curves computed with dose algorithm

These properties show the dose engine and dose engine version used to calculate the dose curves and the absolute dosimetry for uncommissioned machines. Only applicable for PBS and and Line scanning machines.

- IonMonteCarlo - The Monte Carlo (MC) dose engine for proton PBS and Line scanning techniques
- SpotWeightPencilBeam - The Pencil beam (PB) dose engine for proton PBS and Line scanning techniques
- CarbonPencilBeam - The Pencil beam (PB) dose engine for carbon PBS techniques

The dose engine version major and minor numbers are indicated after the dose engine name. Please refer to the *RSL-D-RS-9A-REF, RayStation 9A Reference Manual* for detailed information about the dose engines and dose engine versions used in RayStation.

Commissioned by / Commission time

These properties will be shown for commissioned machines and indicates the last time the machine was commissioned and by which user.

Commissioned for dose algorithm

These properties show the dose engine and dose engine version used to calculate the dose curves and the absolute dosimetry for commissioned machines.

- IonMonteCarlo - The Monte Carlo dose engine used for final dose calculation for proton PBS and Line scanning techniques
- SpotWeightMonteCarlo - The Monte Carlo dose engine used for optimization for proton PBS and Line scanning techniques

The machines will be commissioned for both IonMonteCarlo and SpotWeightMonteCarlo if dose curves and absolute dosimetry have been computed with IonMonteCarlo.

- SpotWeightPencilBeam - The Pencil beam (PB) dose engine used for optimization and final dose calculation for proton PBS and Line scanning techniques
- CarbonPencilBeam - The Pencil beam (PB) dose engine used for optimization and final dose calculation for carbon PBS techniques
- IonPencilBeam - The Pencil beam (PB) dose engine used for final dose calculation for proton Uniform Scanning (US), Double scattering (DS) and Wobbling techniques

The dose engine version major and minor numbers are indicated after the dose engine name. Please refer to the *RSL-D-RS-9A-REF, RayStation 9A Reference Manual* for detailed information about the dose engines and dose engine versions used in RayStation.

Primary dosimeter unit

Indicates whether Monitor Units (MU) or Number of Particles (NP) should be used as primary dosimeter unit for the machine.

Machine design

This property describes the machine design set in the machine. It is used to control machine behavior in RayStation specific for a certain machine vendor. The name is also exported in the DICOM tag "Manufacturer (0008,0070)" for setup beams in the RT Ion Plan.

Manufacturer's model name

This name will be exported in the DICOM tag "Manufacturers model name (0008,1090)" in the ion beam sequence in the RT Ion Plan.

Dose type

This property sets whether the machine is configured according to physical absorbed dose (PHY) or photon-equivalent dose (RBE). The Dose type property shall only be set to RBE if the Absolute dosimetry measurements used to create the beam model were scaled with a constant RBE scale factor of 1.1 prior to the import in RayPhysics.

- Machines with Dose type **PHY** must be used in combination with an RBE model in RayStation. It is possible to view and DICOM export both RBE and physical doses for plans created with such machines in RayStation. QA doses and BDSP doses are displayed and DICOM exported as physical doses.
- Machines with Dose Type **RBE** are assumed to have a constant scale factor of 1.1 included in the absolute dosimetry calibration and can not be used in combination with RBE models in RayStation. It is only possible to view and DICOM export RBE doses for plans created with such machines in RayStation. Note that also QA doses and BDSP doses are displayed and DICOM exported as RBE doses.

Perform the following steps to switch from Dose Type **RBE** to Dose type **PHY** and update the beam model:

1. Optionally: Export the Absolute dosimetry measurements according to *Export curves on page 288*.
2. Remove the Absolute dosimetry measurements according to *Remove curves on page 289*. Note that this will not invalidate the existing beam model.
3. Change the Dose Type property to **PHY**. Note that this will not invalidate the existing beam model.
4. Import new Absolute dosimetry measurements relating to physical dose according to *Import curves on page 288*. The file format is described in *section B.2.5 Ion treatment machines on page 386*. Optionally the Absolute dosimetry measurement file exported in step 1 can be re-used after downscaling of the measurements to physical dose. Note that this will not invalidate the existing beam model.
5. Launch the automodeling process according to *Launch auto-modeling on page 291* to update the beam model with respect to the Absolute dosimetry measurements related to physical dose.

RBE scale factor for Dose type RBE

The scale factor between physical absorbed dose and photon-equivalent dose used to scale the Absolute dosimetry measurements prior to import in RayPhysics. Displayed for machines with Dose Type RBE. Note that the scale factor is assumed to be 1.1 and that it is the user responsibility to validate that this is correct for the imported Absolute dosimetry measurements used for the beam model.

Patient support ID

The Patient support ID will be exported in the DICOM tag "Patient support ID, (300A,0352)" in the ion beam sequence in the RT Ion Plan. If left blank, the default "TABLE" will be exported.

Room view model

This selection decides how the machine is visualized in the Room View. For Ion treatment machines the room view will always only display the couch ("Only couch").

Supported gantry angles (start, stop) [deg]

This property sets the allowed angles for radiation treatment. Angles must be in the interval 0 to 360 deg. Only one angular interval can be set up. Allowed angles range from start to stop towards increasing angles. If the start angle is larger than the stop angle, the interval from start to 360 deg and from 0 deg to stop is allowed. For start angle 181 deg and stop angle 179 deg this gives an allowed gantry angle interval between 181 to 360 deg and 0 to 179 deg. If all angles are allowed, check the **Allow all gantry angles** checkbox.

For machines machines with multiple discrete gantry angles with different beam models, the **Supported discrete gantry angle interval** must be set so that it covers all discrete gantry angles in the machine. For machines with a single discrete gantry angle, the **Supported discrete gantry angle interval** should be set to the same value for start and stop, i.e., start 90 deg and stop 90 deg.

Note: *In RayPhysics, it is only allowed to perform automodel and compute dose for gantry angles 0 and 90 deg. For machines with a single discrete gantry angle different than 0 or 90 deg, the Supported discrete gantry angle interval can be set temporarily to allow all gantry angles before automodel and dose curve computation, and then changed to the fixed gantry angle as a last step.*

Supported collimator angles (start, stop) [deg]

This property sets the allowed collimator angles for radiation treatment. The logic works the same as the gantry angles described above. Collimator angles different from zero are not supported for carbon ion machines or Mevion HYPERSCAN.

Supported couch rotation angles (start, stop) [deg]

This property sets the allowed couch rotation angles for radiation treatment. The logic works the same as the gantry angles described above.

Couch pitch angles (start, stop) [deg]

This property sets the allowed couch pitch angles for radiation treatment. The logic works the same as the gantry angles above.

Couch roll angles (start, stop) [deg]

This property sets the allowed couch roll angles for radiation treatment. The logic works the same as the gantry angles above.

The couch coordinate system

For Ion treatment machines the only supported couch coordinate system is IEC 61217. The couch rotation angle is zero when the head is towards the gantry in the head first orientations. The couch angle increases counter-clockwise when looking from above.

The pitch angle of the couch is zero when the patient is lying flat on the couch. Positive rotation direction is such that the head of an HFS (Head First Supine) patient is raised higher than the feet.

The roll angle of the couch is zero when the patient is lying flat on the couch. Positive rotation direction is such that the right side of an HFS (Head First Supine) patient is raised higher than the left side.

The gantry and collimator coordinate system

For Ion treatment machines the only supported gantry coordinate system is IEC 61217. The IEC 61217 gantry coordinate system has gantry angle zero when the beam enters from above and positive rotation direction clockwise when facing the gantry.

6.1.2 Beam line objects

This section describes the **Beam line objects** tab in the Ion treatment machine properties workspace.

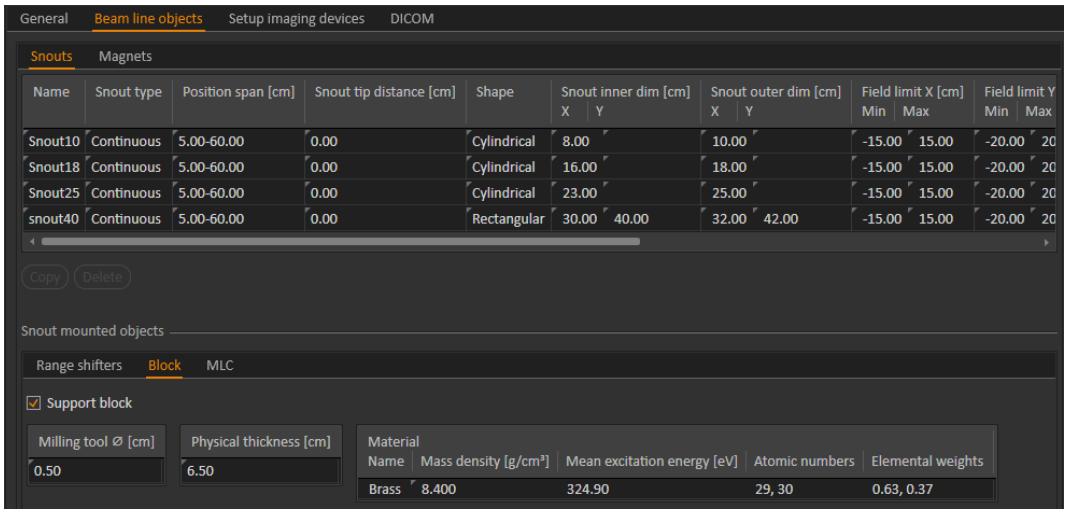


Figure 112. The **Beam line objects** tab in the Machine properties workspace where the **Block** tab is active.

Snouts

The **Snouts** table lists the available snouts for the selected Ion treatment machine. There is also information about the allowed snout positions and relations to other beam line objects mounted in connection to the snout. Downstream refers to to a position closer to the patient, while upstream refers to a position closer to the source along the Z axis (IEC 61217 machine coordinate system).

In RayStation, applicators are modeled as snouts. The following properties can be set for each snout:

- **Name** - the snout name. This will be displayed in RayStation for selection of snout for each beam. The snout name will also be exported in the DICOM RT Ion Plan in the Snout ID (300A,030F) tag or the Applicator ID (300A,0108) tag.
- **Snout type** - indicates whether the snout has a fixed, discrete or continuous position span.
- **Position span [cm]** - sets the allowed snout position span along the Z axis (IEC 61217 machine coordinate system). For continuous snout types, minimum and maximum snout positions are entered. For fixed and discrete snout types, the allowed snout position(s) are entered. The snout position is defined as the distance from the isocenter to the snout position plane defined in the treatment machine.
- **Snout tip distance [cm]** - the distance from the snout position plane to the most downstream part of the snout along the Z axis (IEC 61217 machine coordinate system). The distance must be zero or negative, i.e., the snout tip is either at the snout position plane or downstream of the snout position plane. The snout tip distance is used for collision control.

- **Shape** - indicates if the shape of the snout is cylindrical or rectangular. The same shape is used for both the inner and the outer dimensions of the snout.
- **Snout inner dimensions [cm]** - specifies the snout inner dimensions at the most downstream part of the snout, i.e., at the snout tip plane. The X and Y directions (IEC 61217 Beam limiting device coordinate system) are input parameters if the snout shape is rectangular. If the snout shape is cylindrical, the diameter is the only input parameter. The inner dimension will affect the spot positioning for PBS and Line scanning machines. For more information, see *Spot selection (ion PBS and Line Scanning) on page 268*. The snout inner dimension will also place limits on openings created by block or MLC.

  The snout inner dimensions must be set at least 2 mm smaller than the MLC Maximum tip position as projected to the same plane by using Focal Length in X and Y. This margin ensures that MLC leaves in their most retracted position are outside the snout inner dimensions for all collimator angles, and therefore do not influence the dose.

  The snout inner dimension must also be set so that the outermost leaf edges of the MLC leaves are outside the snout inner dimensions as projected by the same plane by using Focal Length in X and Y.
- **Snout outer dimensions [cm]** - specifies the snout outer dimensions at the most downstream part of the snout, i.e. at the snout tip plane. The X and Y directions (IEC 61217 Beam limiting device coordinate system) are input parameters if the snout shape is rectangular. If the snout shape is cylindrical, the diameter is the only input parameter. The outer dimension will be used in air gap computation and collision detection. For more information, see *Air gap computation and collision detection on page 269*. The outer dimension could also affect the proton Monte Carlo dose computation. For more information, please refer to *Dose computation including snout mounted objects on page 268*.
- **Field limit X [cm]** - defines the (largest) deliverable field (X direction), as projected on the isocentric plane (IEC 61217 Gantry coordinate system). The field limits will affect the spot positioning. For more information, see *Spot selection (ion PBS and Line Scanning) on page 268*.
- **Field limit Y [cm]** - defines the (largest) deliverable field (Y direction), as projected on the isocentric plane (IEC 61217 Gantry coordinate system). The field limits will affect the spot positioning. For more information, see *Spot selection (ion PBS and Line Scanning) on page 268*.
- **Range shifter** - visible if the machine supports range shifters.
  - **Supported** set to "Optional" indicates that it is optional to use a range shifter for the snout.
  - **Supported** set to "No" indicates that the snout does not support range shifters.
  - **Tray distance [cm]** - the distance from the snout position plane to the virtual tray of the range shifter along the Z axis (IEC 61217 Machine coordinate systems). A negative value means that the tray is downstream of the snout position plane, and a positive value that it is upstream of the snout position plane.
- **Compensator** - visible if the machine supports compensators.

  - **Supported** set to "Optional" indicates that it is optional to use a compensator for the snout.
  - **Supported** set to "No" indicates that the snout does not support compensators.
  - **Supported** set to "Required" indicates that a compensator is required for the snout.
  - **Mounting** - indicates how the compensator is mounted on the tray. Only source-sided compensators are supported in RayStation, i.e., the virtual tray is located on the downstream plane of the compensator along the Z axis (IEC 61217 Machine coordinate systems).
  - **Tray mounting** set to "Fixed" indicates that the compensator has a fixed tray position.
  - **Tray mounting** set to "Downstream of block" indicates that the tray position will depend on the thickness of the block created in RayStation, and the value entered in tray position will have no effect.
  - **Tray distance [cm]** - the distance from the snout position plane to the virtual tray of the compensator along the Z axis (IEC 61217 Machine coordinate systems). A negative value means that the tray is downstream of the snout position plane, and a positive values that it is upstream of the snout position plane.

- **Block** - visible if the machine supports blocks.
  - **Supported** set to "Optional" indicates that it is optional to use a block for the snout.
  - **Supported** set to "No" indicates that the snout does not support blocks.
  - **Supported** set to "Required" indicates that a block is required for the snout.
  - **Mounting** - indicates how the block is mounted on the tray along the Z axis (IEC 61217 Machine coordinate systems). It is only allowed to commission machines with source-sided blocks, i.e. where the virtual tray is located on the downstream plane of the block.
  - **Tray distance [cm]** - the distance from the snout position plane to the virtual tray of the block along the Z axis (IEC 61217 Machine coordinate systems). A negative value means that the tray is downstream of the snout position plane, and a positive values that it is upstream of the snout position plane.

- **MLC opening [cm]** - visible if the machine supports MLC to be used for snouts where the MLC shall be set to be used as a secondary collimator for beams with blocks. The MLC opening will be set in the beam as close as possible to the specified X and Y values (IEC 61217 beam limiting device coordinate system). Alternatively the property **MLC to bounding box margin** in the **MLC** tab can be set for a dynamic MLC opening that is updated according to the block contour.
- **MLC Tray distance [cm]** - Visible if the machine supports MLC. The distance from the snout position plane to the downstream surface of the MLC along the Z axis (IEC 61217 Machine coordinate systems). A negative value means that the MLC downstream surface is downstream of the snout position plane, and a positive values that it is upstream of the snout position plane.

- **Export as applicator** - used to indicate if the snout properties should be DICOM exported in the Applicator sequence (300A,0107) instead of the Snout sequence (300A,030C).

Range modulators/Ridge filters

The **Range modulators/Ridge filters** table lists the available range modulators/ridge filters for the selected machine. The term "Ridge filter" is used if the selected range modulator(s) type is fixed, otherwise the standard "Range modulator" terminology is used throughout this view.

The following properties are displayed for each range modulator/ridge filter:

- **Name** - the range modulator/ridge filter name (editable).
- **Description** - the range modulator/ridge filter description (editable).
- **Type** - indicates whether the range modulator/ridge filter type is "Fixed", "Wheel Fixed Weights" or "Wheel Modulated Weights" (editable).
- **Isocenter To Tray Distance [cm]** - the isocenter to tray distance along the Z axis (IEC 61217 Machine coordinate systems).

In addition to these properties, it is possible to display further information for each selected range modulator/ridge filter in the table:

- **Step water equivalent thickness [cm]** – visible if the range modulator/ridge filter has a defined step water equivalent thickness.
- **Material** – visible if the range modulator/ridge filter has a defined material.

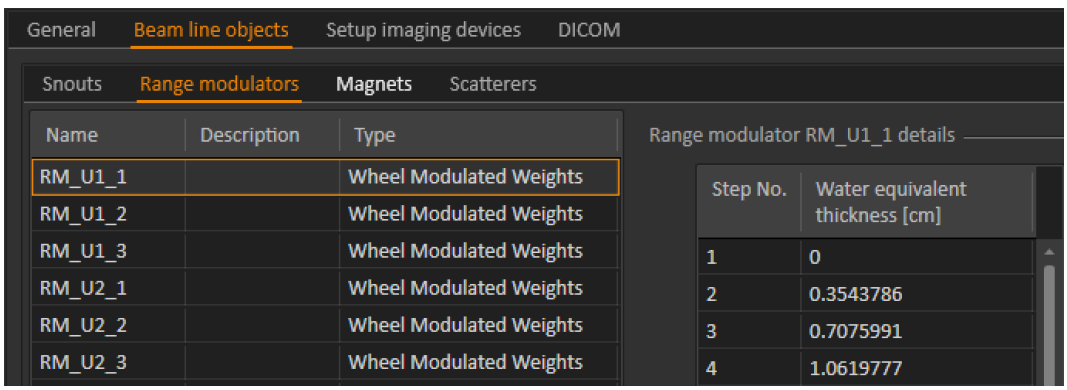


Figure 113. The **Beam line objects** tab in the Machine constraints workspace where the **Range modulators** tab is active.

Scatterers

The **Scatterers** tab is visible only if the machine has scatterers.

The following properties are visible:

- For first scatterers: **Name**, **Physical thickness [cm]**, **Isocenter to tray distance [cm]** and **Material**.
- For lollipops: **Name**, **Physical thickness [cm]**, **Water equivalent thickness [cm]**, **Upstream face to tray distance [cm]** and **Material**.
- For second scatterers: **Name**, **Water equivalent thickness [cm]** and **Isocenter to tray distance [cm]**.

All thicknesses and distances for scatterers are defined along the Z axis (IEC 61217 Machine coordinate systems).

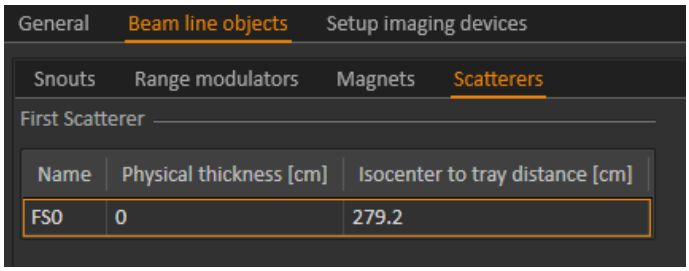


Figure 114. The **Beam line objects** tab in the Machine constraints workspace where the **Scatterers** tab is active.

Lateral spreading devices/Magnets

In the **Lateral spreading devices** or **Magnets** tab the user can select if the RT Ion plans created for the machine shall contain information about Magnets by checking the **Define magnets for DICOM export** and/or the **Define scatterer for DICOM export** checkbox. The **Define scatterer for DICOM export** checkbox is only available in the case of beam delivery type Pencil Beam Scanning and Line Scanning, in which case the tab header will be named **Lateral spreading devices**. Enter information about magnets or scatterer if any external system receiving the RTIonPlan from RayStation needs them to be defined in the Lateral Spreading Device Sequence (300A,0332). If a checkbox is left unchecked the RTIonPlan will not include the corresponding magnets or scatterer in the Lateral Spreading Device Sequence (300A,0332) and the Lateral Spreading Device Settings Sequence (300A,0370).

The following properties can be defined for magnets:

- **Device name** - DICOM exported as Lateral Spreading Device ID (300A,0336). The magnets and/or scatterer must have unique names.
- **Isocenter to device distance [cm]** - DICOM exported as Isocenter to Lateral Spreading Device Distance (300A,0374)
- **Lateral spreading device setting** - DICOM exported as Lateral Spreading Device Setting (300A,0372)
- **Water equivalent thickness [cm]** - DICOM exported as Lateral Spreading Device Water Equivalent Thickness (300A,033C)

The values are only used to populated the tags in the DICOM export and are not used in RayStation.

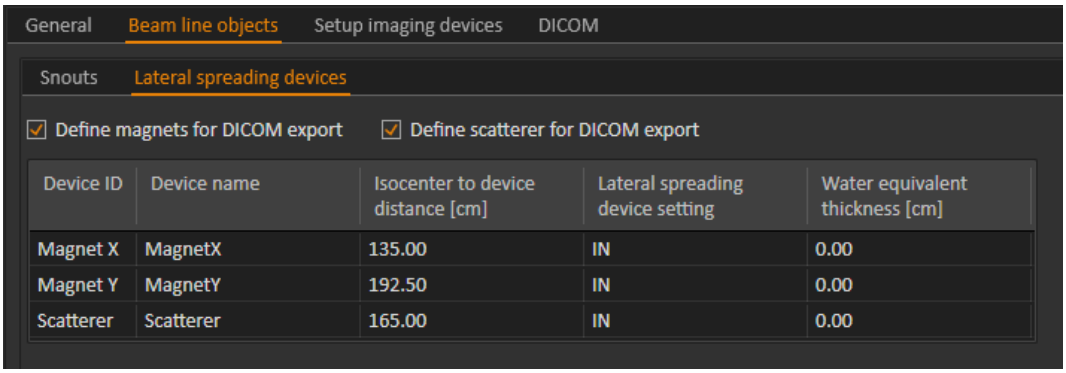


Figure 115. The **Beam line objects** tab in the Machine constraints workspace where the **Lateral spreading devices** tab is active.

Snout mounted objects - range shifters

The **Range shifters** tab lists the available range shifters and their properties for the selected Ion treatment machine, if the machine supports range shifters.

The following properties can be set for a range shifter:

- **Name** - the range shifter name. This will be displayed in RayStation for selection of range shifter for each beam. The range shifter name will also be exported in the DICOM RT Ion Plan in the tag Range Shifter ID (300A,0318).
- **Mounting position** - the distance from the snout position plane to the virtual tray of the range shifter along the Z axis (IEC 61217 Machine coordinate systems). The following mounting positions are supported: Source side or Patient side.
- **Physical thickness [cm]** - Defines the physical thickness of the range shifter along the Z axis (IEC 61217 Machine coordinate systems).
  - **WET [cm]** - Visible for certain passive machines that has range shifters in the nozzle. Used to set water equivalent thickness [cm] instead of **Physical thickness [cm]**.
  - **Isocenter to tray distance [cm]** - The isocenter to tray distance along the Z axis (IEC 61217 Machine coordinate systems). Mandatory for machines where **WET [cm]** is defined.
- **Shape** - indicates if the shape of the range shifter is cylindrical or rectangular. If not specified, the range shifter will inherit the snout outer dimensions. The values will affect spot positioning (see *Spot selection (ion PBS and Line Scanning) on page 268*), dose computation for proton Monte Carlo (see *Dose computation including snout mounted objects on page 268*) and air gap/collision detection (see *Air gap computation and collision detection on page 269*).
- **Lateral dimensions [cm]** - (IEC 61217 beam limiting device coordinate system) If not specified, the range shifter will inherit the snout outer dimensions. The values will affect spot positioning (see *Spot selection (ion PBS and Line Scanning) on page 268*) , dose computation for proton

Monte Carlo (see *Dose computation including snout mounted objects on page 268*) and air gap/collision detection (see *Air gap computation and collision detection on page 269*).

- **Material, Name** - The range shifter material can be selected from a predefined list of materials, including PMMA, Lexan, Polyethylene and ABT Resin.
- **Material, Mass density** - The mass density can be edited, but the material composition and ionization energy are fixed.

Note: *If the range shifter WET has been measured, it is possible to adjust the density of the material so that the WET in the machine model matches the measured WET.*

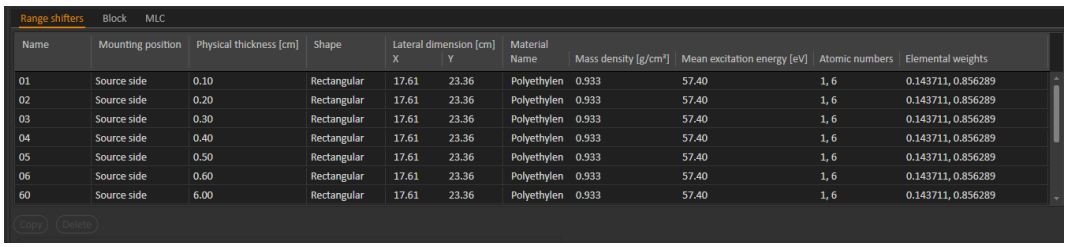

Range shifters
Block
MLC
Name
Mounting position
Physical thickness [cm]
Shape
Lateral dimension [cm]
X
Y
Material
Name
Mass density [g/cm³]
Mean excitation energy [eV]
Atomic numbers
Elemental weights
01 Source side 0.10 Rectangular 17.61 23.36 Polyethylen 0.933 57.40 1, 6 0.143711, 0.856289
02 Source side 0.20 Rectangular 17.61 23.36 Polyethylen 0.933 57.40 1, 6 0.143711, 0.856289
03 Source side 0.30 Rectangular 17.61 23.36 Polyethylen 0.933 57.40 1, 6 0.143711, 0.856289
04 Source side 0.40 Rectangular 17.61 23.36 Polyethylen 0.933 57.40 1, 6 0.143711, 0.856289
05 Source side 0.50 Rectangular 17.61 23.36 Polyethylen 0.933 57.40 1, 6 0.143711, 0.856289
06 Source side 0.60 Rectangular 17.61 23.36 Polyethylen 0.933 57.40 1, 6 0.143711, 0.856289
60 Source side 6.00 Rectangular 17.61 23.36 Polyethylen 0.933 57.40 1, 6 0.143711, 0.856289
Copy
Delete

Figure 116. The **Snout mounted objects** area in the Machine constraints workspace where the **Range shifters** tab is active for PBS/LS.

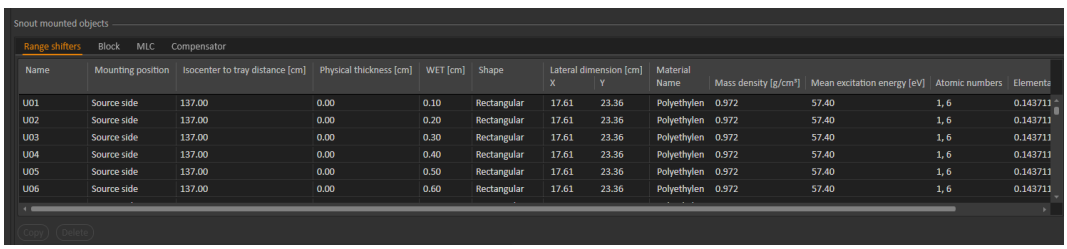

Snout mounted objects
Range shifters
Block
MLC
Compensator
Name
Mounting position
Isocenter to tray distance [cm]
Physical thickness [cm]
WET [cm]
Shape
Lateral dimension [cm]
X
Y
Material
Name
Mass density [g/cm³]
Mean excitation energy [eV]
Atomic numbers
U01 Source side 137.00 0.00 0.10 Rectangular 17.61 23.36 Polyethylen 0.972 57.40 1, 6
U02 Source side 137.00 0.00 0.20 Rectangular 17.61 23.36 Polyethylen 0.972 57.40 1, 6
U03 Source side 137.00 0.00 0.30 Rectangular 17.61 23.36 Polyethylen 0.972 57.40 1, 6
U04 Source side 137.00 0.00 0.40 Rectangular 17.61 23.36 Polyethylen 0.972 57.40 1, 6
U05 Source side 137.00 0.00 0.50 Rectangular 17.61 23.36 Polyethylen 0.972 57.40 1, 6
U06 Source side 137.00 0.00 0.60 Rectangular 17.61 23.36 Polyethylen 0.972 57.40 1, 6
Copy
Delete

Figure 117. The **Snout mounted objects** area in the Machine constraints workspace where the **Range shifters** tab is active for US/DS/Wobbling.

Snout mounted objects - block

In the **Block** tab, the user can select if the machine supports blocks. For a machine that supports blocks, it is possible to specify the following properties:

- **Milling tool Ø [cm]** - Physical diameter of the available block milling tools. Used as a post processing step in the block contour generation in RayStation to ensure the resulting block contour is manufacturable. The Milling tool diameter must be 0.1 cm or larger to affect the block contour in RayStation.
- **Physical thickness [cm]** - Defines the available physical thicknesses of the blocks along the Z axis (IEC 61217 Machine coordinate systems).

- **Material** - The block material is always brass with predefined material properties. The mass density can be edited. The material properties will be used in the PBS and Line scanning Monte Carlo dose engine for beams with block apertures.

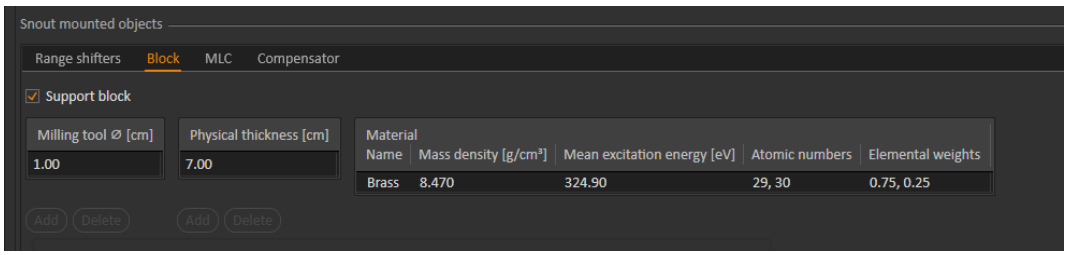


Figure 118. The **Snout mounted objects** area in the Machine constraints workspace where the **Block** tab is active.

Snout mounted objects - MLC

In the **MLC** tab the user can select if the machine supports MLC by checking the **Has MLC** checkbox. Only MLC moving in the X direction (IEC 61217 Beam limiting device coordinate system) is supported.

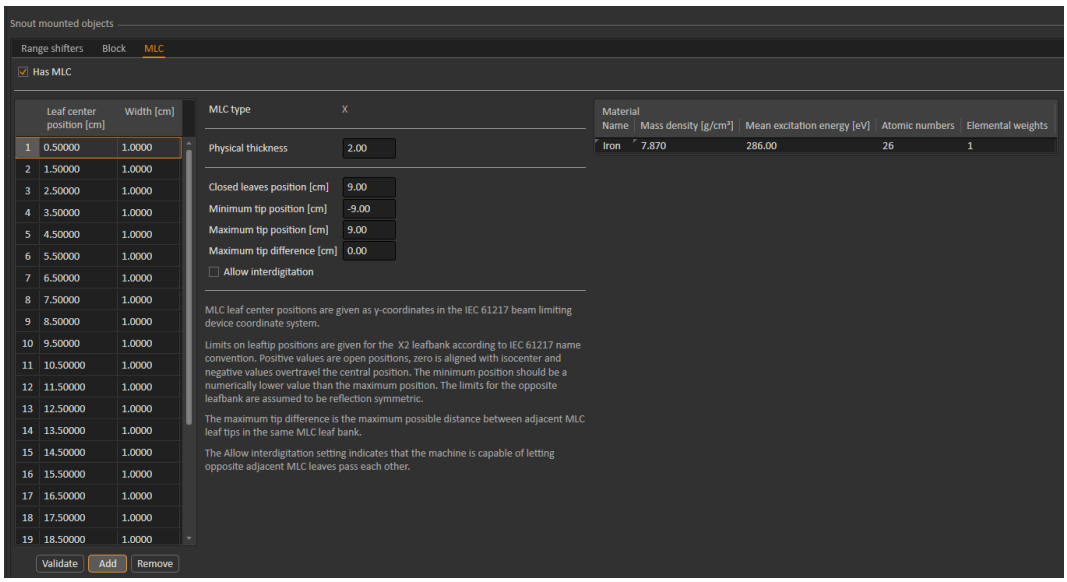

Snout mounted objects
Range shifters
Block
MLC
Has MLC
Leaf center position [cm]
Width [cm]
MLC type
X
Physical thickness
2.00
Closed leaves position [cm]
9.00
Minimum tip position [cm]
-9.00
Maximum tip position [cm]
9.00
Maximum tip difference [cm]
0.00
Allow interdigitation
Material
Name
Mass density [g/cm³]
Mean excitation energy [eV]
Atomic numbers
Elemental weights
Iron
7.870
286.00
26
1
MLC leaf center positions are given as y-coordinates in the IEC 61217 beam limiting device coordinate system.
Limits on leaftip positions are given for the X2 leafbank according to IEC 61217 name convention. Positive values are open positions, zero is aligned with isocenter and negative values overtravel the central position. The minimum position should be a numerically lower value than the maximum position. The limits for the opposite leafbank are assumed to be reflection symmetric.
The maximum tip difference is the maximum possible distance between adjacent MLC leaf tips in the same MLC leaf bank.
The Allow interdigitation setting indicates that the machine is capable of letting opposite adjacent MLC leaves pass each other.
Validate
Add
Remove

Figure 119. The **Snout mounted objects** area in the Machine constraints workspace where the **MLC** tab is active.

The user can specify the following properties for the MLC geometry:

- **Leaf center position and width** - The MLC table to the left in the **MLC** tab lists the leaves and their position and width. The properties in this table are applied to both the left and right MLC leaves of an MLC leaf pair. The number of leaves entered should be the number of leaf pairs,

which is half of the total number of leaves. The **Leaf center position [cm]** entry describes the center position of the leaves along the y-axis of the IEC61217 Beam limiting device coordinate system. The **Width [cm]** entry describes the width of the individual MLC leaf in question, along the same axis as the center positions. The leaf center positions and widths are given on the physical MLC plane.

Note: *DICOM-export of leaf positions indicates the edge position of the leaf and not the central position, as in this table.*

- **Remove** - MLC leaves marked in the table are deleted with the **Remove** button.
- **Add** - Click the **Add** button to open a dialog to add new leaves to the table. In the Add leaves dialog the **Number of leaves** is the number of leaves to be generated. **Leaf center start position [cm]** defines the center position of the first leaf in cm. **Width [cm]** defines the width of a single leaf. Some machines have MLC with two different leaf widths. If this is the case, the different leaf regions must be added separately.

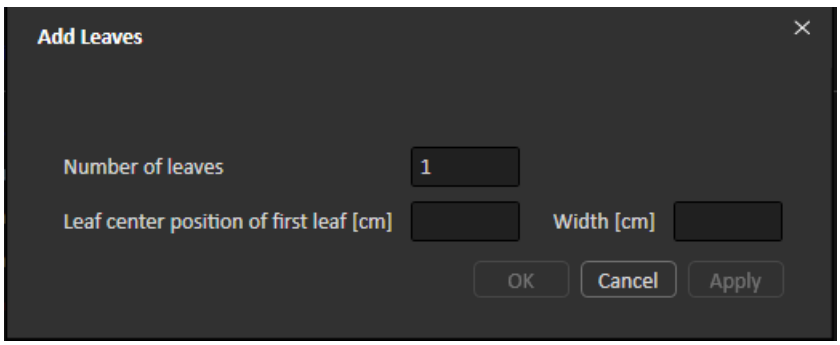


Figure 120. The **Add Leaves** dialog.

- **Validate** - Click the **Validate** button to validate that there are no overlaps or holes in the MLC-setup.
- **Physical thickness [cm]** - Defines the physical thickness of the MLC along the Z axis (IEC 61217 Machine coordinate systems).

The following properties relating to MLC movement restrictions in the X direction (IEC 61217 beam limiting device coordinate system) can be set:

- **Default closed leaves position [cm]** - the default position where a closed leaf pair meet. If the leaves cannot close at the default position, they will close as far away from the central axis as possible.
- **Minimum tip position [cm]** - the position of the MLC where the leaf over-travels the axis the most, or is closest to the central axis if over-travel is not allowed; -5 cm means that the MLC-leaves (both left and right leaf bank) can move 5 cm past the central axis. The property is symmetric for the two leaf banks.

- **Maximum tip position [cm]** - the most open allowed position of the MLC leaves; 20 cm means that the MLC-leaves (both left and right) can move 20 cm out from the central axis. The property is symmetric for the two leaf banks.
- **Maximum tip difference [cm]** - the maximum possible distance between adjacent MLC leaf tips in the same MLC leaf bank.
- **Allow interdigitation** - this setting indicates that the machine is capable of letting opposite adjacent MLC leaves pass each other. For example, if leaf number i in the left leaf bank is 4 cm away from the isocenter axis, leaf i+1 in the right leaf bank is still allowed to over-travel by more than 4 cm.
- **Margin to block bounding box** - visible only for machines where this property is set. This parameter is only supported for US/DS/Wobbling. Optional parameter to use for a dynamic MLC opening when the MLC leaves should be used as a secondary collimator to avoid leakage when using blocks. If this property is used the MLC leaves will form a bounding box around the block contour with the specified margin. Alternatively the **MLC opening** in the snout list can be set to form a static opening.
- **Material table** - the supported MLC materials are iron or brass with predefined material properties. The density can be edited. The material properties will be used in the PBS and Line scanning Monte Carlo dose engine for beams with MLC apertures.

Snout mounted objects - compensator

In the Compensator tab, the user can select if the machine supports compensators. For a machine that supports compensators, it is possible to specify the following properties that is used for compensator creation in RayStation. Details on how the compensator is created are found in the Compensator section in the *RSL-D-RS-9A-REF, RayStation 9A Reference Manual*.

- **Minimum physical thickness [cm]** - Specifies the minimum allowed physical thickness of the compensator along Z axis (IEC 61217 Machine coordinate systems).
- **Maximum physical thickness [cm]** - Specifies the maximum allowed physical thickness of the compensator along Z axis (IEC 61217 Machine coordinate systems).
- **Default maximum physical thickness [cm]** - Specifies the default maximum physical thickness of the compensator along Z axis (IEC 61217 Machine coordinate systems). Should be smaller or equal to the **Maximum physical thickness**.
- **Milling grid pattern** - Regular or Hexagonal. Specifies the milling pattern for the compensator.
- **Milling tool diameter Ø [cm]** - Physical diameter(s) of the available compensator milling tools.
- **Material** - The compensator material and the material properties are predefined. The density can be edited.

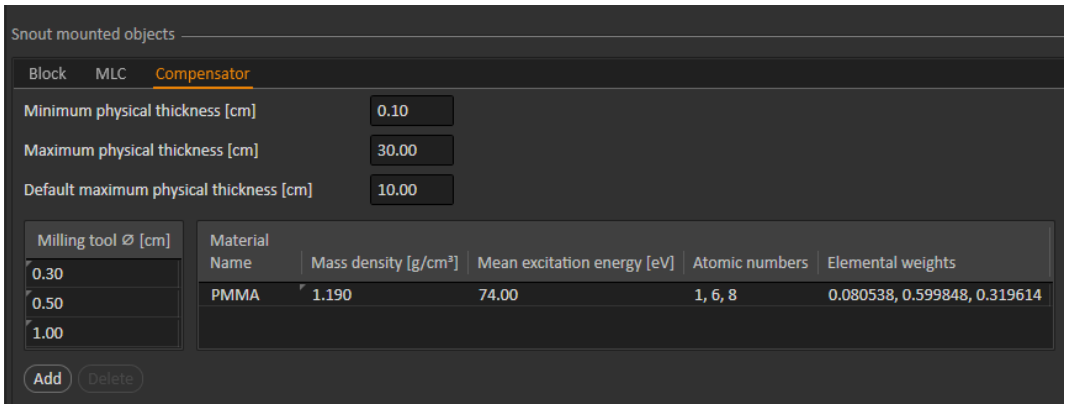
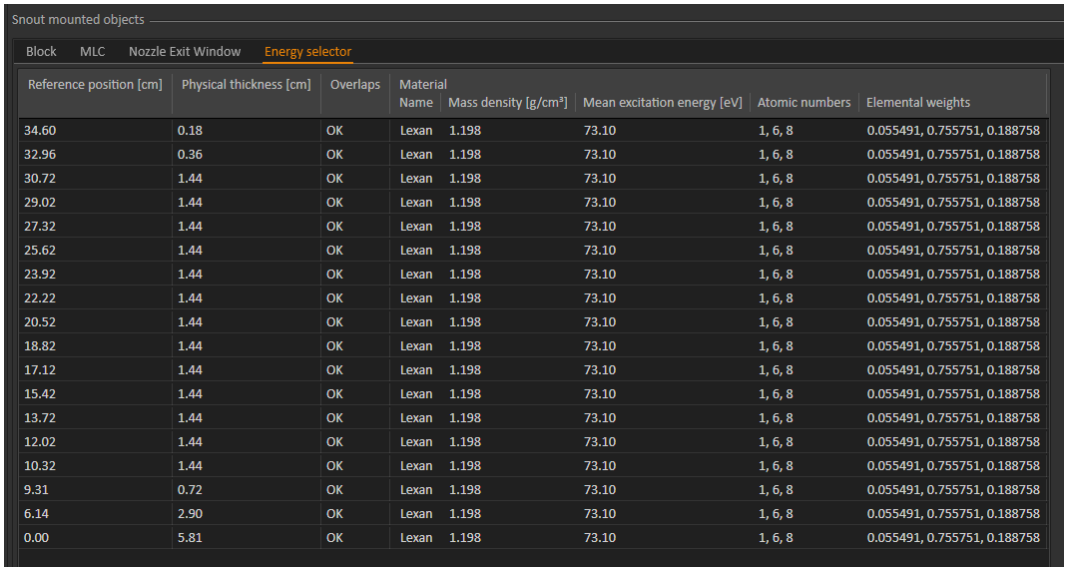


Figure 121. The **Snout mounted objects** area in the Machine constraints workspace where the **Compensator** tab is active.

Snout mounted objects - energy selector

The **Energy selector** tab is visible for machines where the energy selection system is part of the beam line geometry as a binary range shifter i.e. for Mevion Hyperscan machines. Each range shifter plate can be defined with a given position along the energy selector, a material and an (editable) mass density.

Each energy of the machine is associated with a binary sequence (see *Supported energies on page 276*), specifying which of the plates are inserted into the beam line. The order of this sequence corresponds to the geometrical ordering of the plates from source to patient with the highest reference position closest to the source.



Reference position [cm]	Physical thickness [cm]	Overlaps	Material				
			Name	Mass density [g/cm³]	Mean excitation energy [eV]	Atomic numbers	Elemental weights
34.60	0.18	OK	Lexan	1.198	73.10	1, 6, 8	0.055491, 0.755751, 0.188758
32.96	0.36	OK	Lexan	1.198	73.10	1, 6, 8	0.055491, 0.755751, 0.188758
30.72	1.44	OK	Lexan	1.198	73.10	1, 6, 8	0.055491, 0.755751, 0.188758
29.02	1.44	OK	Lexan	1.198	73.10	1, 6, 8	0.055491, 0.755751, 0.188758
27.32	1.44	OK	Lexan	1.198	73.10	1, 6, 8	0.055491, 0.755751, 0.188758
25.62	1.44	OK	Lexan	1.198	73.10	1, 6, 8	0.055491, 0.755751, 0.188758
23.92	1.44	OK	Lexan	1.198	73.10	1, 6, 8	0.055491, 0.755751, 0.188758
22.22	1.44	OK	Lexan	1.198	73.10	1, 6, 8	0.055491, 0.755751, 0.188758
20.52	1.44	OK	Lexan	1.198	73.10	1, 6, 8	0.055491, 0.755751, 0.188758
18.82	1.44	OK	Lexan	1.198	73.10	1, 6, 8	0.055491, 0.755751, 0.188758
17.12	1.44	OK	Lexan	1.198	73.10	1, 6, 8	0.055491, 0.755751, 0.188758
15.42	1.44	OK	Lexan	1.198	73.10	1, 6, 8	0.055491, 0.755751, 0.188758
13.72	1.44	OK	Lexan	1.198	73.10	1, 6, 8	0.055491, 0.755751, 0.188758
12.02	1.44	OK	Lexan	1.198	73.10	1, 6, 8	0.055491, 0.755751, 0.188758
10.32	1.44	OK	Lexan	1.198	73.10	1, 6, 8	0.055491, 0.755751, 0.188758
9.31	0.72	OK	Lexan	1.198	73.10	1, 6, 8	0.055491, 0.755751, 0.188758
6.14	2.90	OK	Lexan	1.198	73.10	1, 6, 8	0.055491, 0.755751, 0.188758
0.00	5.81	OK	Lexan	1.198	73.10	1, 6, 8	0.055491, 0.755751, 0.188758

Figure 122. The **Snout mounted objects** area in the Machine constraints workspace where the **Energy selector** tab is active.

Snout mounted objects - nozzle exit window

In the **Nozzle Exit Window** tab the user can select if the machine has a nozzle exit window in the beam line. If supported, the window material can be chosen from a pre-defined list. Shape, dimensions, density and physical thickness are editable properties.

The nozzle exit window enters the collision detection similar to a range shifter object.

If the machine is selected to have a nozzle exit window, the window will also be included in the dose computation during beam commissioning. If any of the imported curves include measurements taken without the nozzle exit window, there will be an expected discrepancy between the measured and the computed values. The size of the discrepancy will depend on the dimension and material of the nozzle exit window.

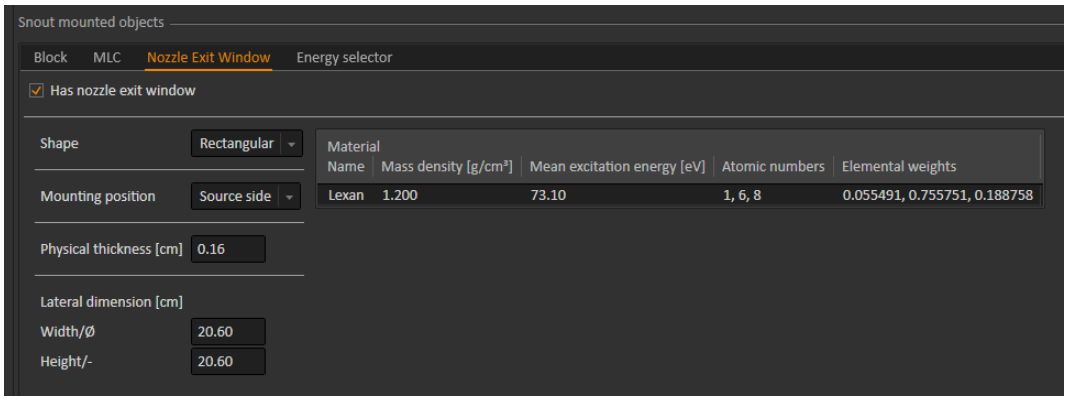


Figure 123. The **Snout mounted objects** area in the Machine constraints workspace where the **Nozzle Exit Window** tab is active.

Beam line

The relations of beam line objects along the Z axis (IEC 61217 Machine coordinate systems) for a machine are illustrated in an image at the bottom of the workspace. The figures illustrate that all tray distances should be measured from the snout position plane, where 0 means that the tray coincides with the snout position plane, a negative value means that the tray is downstream of the snout position plane, and a positive value that the tray is upstream of the snout position plane. Downstream refers to to a position closer to the patient, while upstream refers to a position closer to the source.

The figures also illustrate that a source-sided object has its tray on the downstream surface, while a patient-sided object has its tray on the upstream surface.

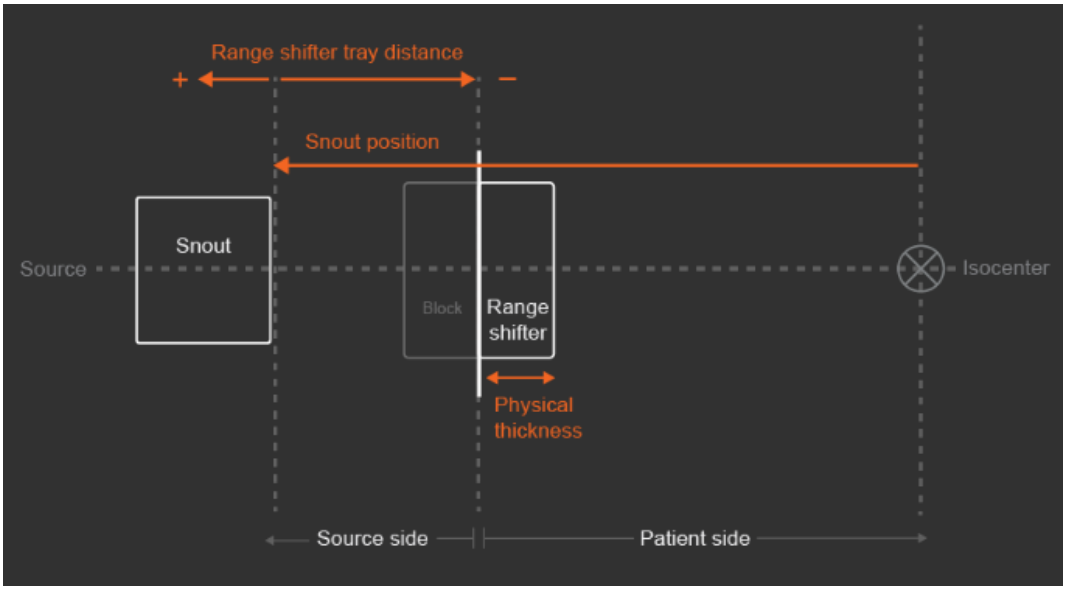


Figure 124. An illustration of the beam line objects where a range shifter is highlighted (the Range shifter tab is active).

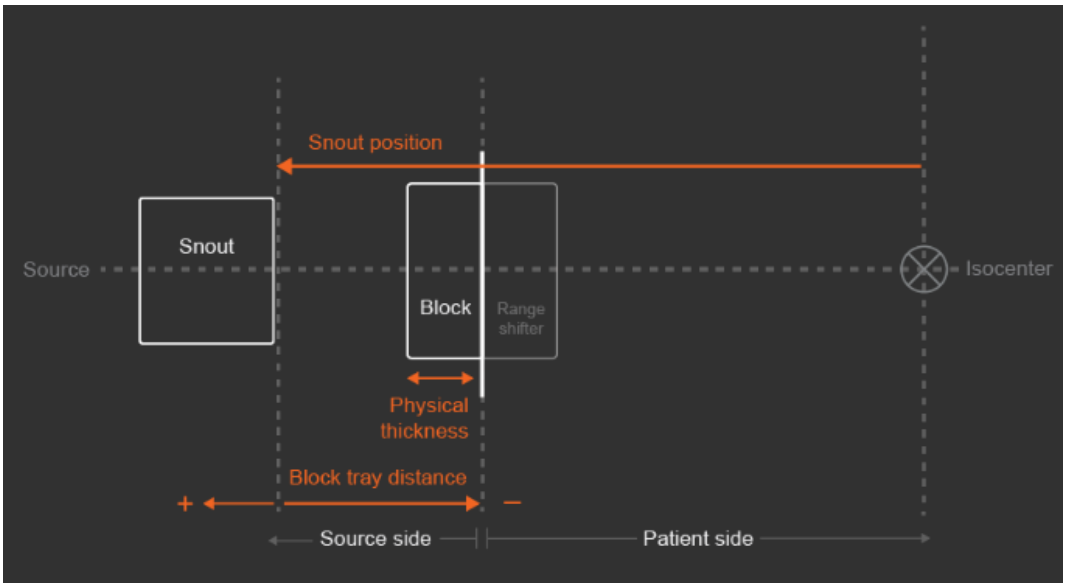


Figure 125. An illustration of the beam line objects where a block is highlighted (the Block tab is active).

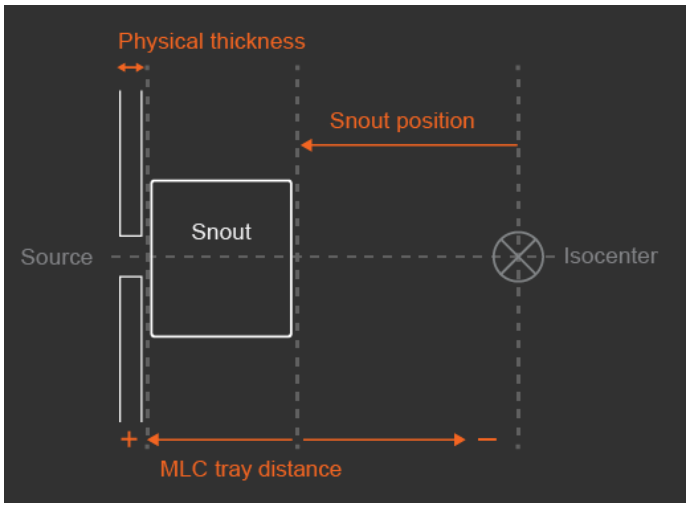


Figure 126. An illustration of the beam line objects where the MLC is highlighted (the MLC tab is active).

Effect of settings for snouts and snout mounted objects in RayStation planning and dose computation

The shape and dimensions of the snouts and snout mounted objects of the machine will affect the spot selection at the start of the optimization, the dose computation and the air gap computation and collision detection.

Spot selection (ion PBS and Line Scanning)

The initial spot positions are set at the start of the optimization in such a way that all spot centers fit inside both the specified field limits and the inner dimensions of the selected snout at the specified location. The inner dimension should therefore be based on the physical dimensions of the snout including a margin, determined by the clinic, not to risk that spots are cropped by the snout.

If a range shifter is used, the region in which spots can be placed is also constrained by the lateral dimensions of the range shifter. In the spot selection algorithm, potential spot positions at isocenter are projected to the downstream surface of the range shifter. If the projected position is within the lateral dimensions of the range shifter minus a safety margin of 1 cm from each border, the spot will be selected to be part of the initial set of spots in the optimization. The range shifter lateral dimensions are by default determined by the snout outer dimensions, but could optionally be assigned in the machine model to individual shapes and dimensions.

The spot selection will also be affected by a block or MLC contour. For more information, refer to the *RSL-D-RS-9A-REF, RayStation 9A Reference Manual*.

Dose computation including snout mounted objects

General algorithm descriptions and handling of snout mounted objects in the Monte Carlo (proton PBS and Line scanning only) and the pencil beam algorithms (carbon PBS and all proton techniques) are described in the *RSL-D-RS-9A-REF, RayStation 9A Reference Manual*. When setting the shape

and dimensions of the snout and snout mounted objects, the following additional information should be considered:

The snout itself is not taken into account in the dose computation, but since most snout mounted objects inherit dimensions from the snout, the chosen snout dimensions will affect the dose computation indirectly.

Range shifters and the nozzle exit window are handled as follows in the dose computation:

- The pencil beam algorithms for carbon ion PBS and for proton PBS and Line scanning will treat range shifters and the nozzle exit window as semi-infinite slabs and the lateral dimensions are disregarded.
- The Monte Carlo algorithm for proton PBS and Line scanning will take the lateral dimensions of the range shifter and nozzle exit window into account explicitly and transport particles through these objects. A particle which intersects the plane of the downstream surface outside the lateral dimensions of the object will not be transported further and will thus not contribute to any dose in the patient. Therefore, the lateral dimensions of the range shifters and nozzle exit window need to be large enough not to lose any relevant part of the spot fluence in the dose computation.

For the Mevion Hyperscan Adaptive Aperture, an active volume defined by the snout outer dimensions and block thickness is used in the dose computation. These dimensions are disregarded in the proton pencil beam algorithm, but are treated in the same way as for the range shifter and the nozzle exit window in the proton Monte Carlo dose computation. This means that the margin between the snout outer and inner dimensions must be large enough to take the full spot fluence into account in the dose computation.

The system has sanity checks before dose computation for the location of the spot center projected to the downstream surface of the following objects:

- Snout: The spot center must fit inside the snout inner dimensions.
- Range shifter: The spot center must fit inside the range shifter dimensions with an additional margin of 1 cm from each border.
- Nozzle exit window: The spot center must fit inside the nozzle exit window with an additional margin of 5 cm from each border.

Since the sanity checks are based only on the location of the spot centers, there is still a risk that large spots lose fluence in the outer regions. It is therefore the responsibility of the user to choose appropriate dimensions for the snouts and snout mounted objects with respect to the properties of the treatment machine.

Air gap computation and collision detection

The air gap calculation and collision detection is performed within the snout outer dimensions and the downstream plane of the most downstream snout mounted object for the selected snout in the beam. This can either be the snout tip, the compensator downstream surface or the range shifter downstream surface, depending on how the machine is commissioned. It is not allowed to

commission machines so that the MLC or block is downstream of the snout tip plane. MLC and block will thus not affect the air gap calculation.

Snout mounted objects inherit lateral shape and outer dimensions from the selected snout for the beam, with the exception of range shifters that can optionally be assigned individual lateral shapes and dimensions during beam commissioning. The gap calculation is performed within these lateral shapes and dimensions.

If present, a nozzle exit window is also taken into account in the air gap computation (similarly to a range shifter).

6.1.3 Setup imaging devices

This section describes the **Setup imaging devices** tab in the Ion treatment machine constraint workspace.

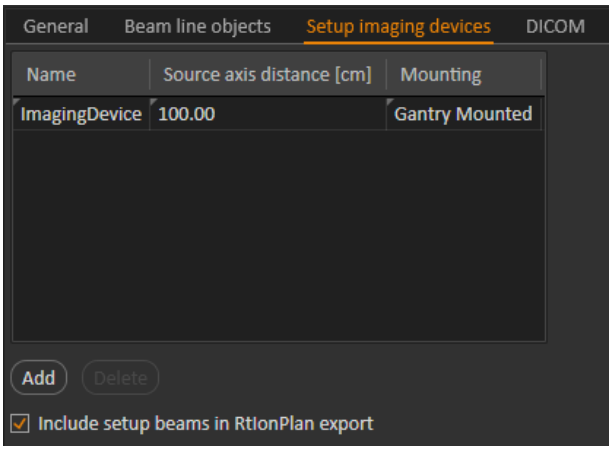


Figure 127. The **Setup imaging devices** tab in the Machine constraints workspace.

It is possible to add new setup imaging devices by clicking the **Add** button and specifying the **Name**, **Source axis distance [cm]** and **Mounting** (Gantry mounted or Fixed).

Select **Include setup beams in RTIonPlan export** by checking the corresponding checkbox, if the setup beams should be exported to DICOM.

Fixed setup imaging devices

If there are fixed setup imaging devices available, as opposed to devices rotating with the gantry, select **Fixed** instead of **Gantry mounted** in the **Mounting** column. Then seven additional columns will be presented, in which the parameters listed below can be entered.

Note: *Non-IEC: Imager rotations are the same as in IEC 61217 Imager System, except that order of the rotations is around: 1) z-axis 2) x-axis 3) y-axis.*

- **Iso-FP [cm]** – Isocenter to Flat panel distance in centimeters.
- **Imager x-pos [cm]** - Imager position in centimeters on x-axis in IEC 61217 Fixed system.
- **Imager y-pos [cm]** - Imager position in centimeters on y-axis in IEC 61217 Fixed system.
- **Imager z-pos [cm]** - Imager position in centimeters on z-axis in IEC 61217 Fixed system.
- **Imager x-rotation [deg]** - Non-IEC: Imager angle in degrees around x-axis. The value will be exported to DICOM as GantryPitchAngle.
- **Imager y-rotation [deg]** - Non-IEC: Imager angle in degrees around y-axis. The value will be exported to DICOM as GantryAngle.

- **Imager z-rotation [deg]** - Non-IEC: Imager angle in degrees around z-axis. The value will not be exported to DICOM.

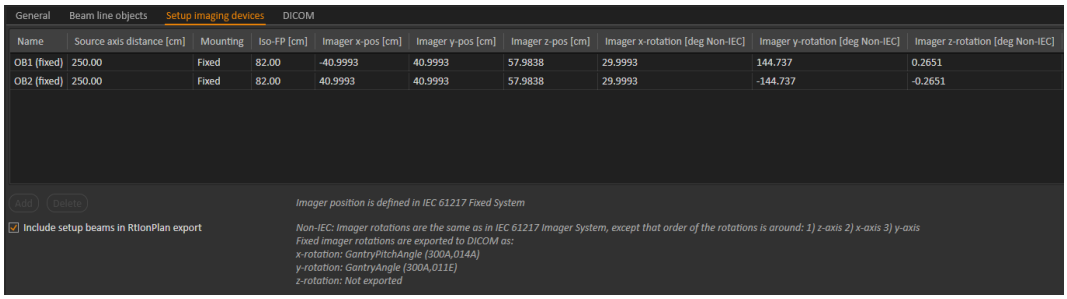

General
Beam line objects
Setup imaging devices
DICOM
Name
Source axis distance [cm]
Mounting
Iso-FP [cm]
Imager x-pos [cm]
Imager y-pos [cm]
Imager z-pos [cm]
Imager x-rotation [deg Non-IEC]
Imager y-rotation [deg Non-IEC]
Imager z-rotation [deg Non-IEC]
OB1 (fixed) 250.00 Fixed 82.00 -40.9993 40.9993 57.9838 29.9993 144.737 0.2651
OB2 (fixed) 250.00 Fixed 82.00 40.9993 40.9993 57.9838 29.9993 -144.737 -0.2651
Add
Delete
Include setup beams in RtionPlan export
Imager position is defined in IEC 61217 Fixed System
Non-IEC: Imager rotations are the same as in IEC 61217 Imager System, except that order of the rotations is around: 1) z-axis 2) x-axis 3) y-axis
Fixed imager rotations are exported to DICOM as:
x-rotation: GantryPitchAngle (300A,014A)
y-rotation: GantryAngle (300A,011E)
z-rotation: Not exported

Figure 128. The **Setup imaging devices** tab in the Machine constraints workspace for fixed setup imaging devices.

6.1.4 DICOM

This section describes the **DICOM** tab in the Ion treatment machine constraint workspace.

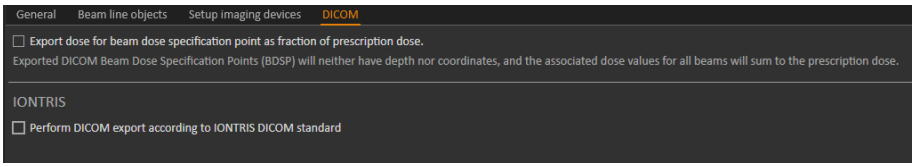

General
Beam line objects
Setup imaging devices
DICOM
Export dose for beam dose specification point as fraction of prescription dose.
Exported DICOM Beam Dose Specification Points (BDSP) will neither have depth nor coordinates, and the associated dose values for all beams will sum to the prescription dose.
IONTRIS
Perform DICOM export according to IONTRIS DICOM standard

Figure 129. The **DICOM** tab in the Machine constraints workspace.

If the **Export dose for beam dose specification point as fraction of prescription dose** is checked, the Beam Dose Specification Point (BDSP) dose will be exported as a fraction of the prescription (not according to DICOM standard). The sum of BDSP dose over all beams and fractions will equal the prescription dose. The BDSP dose will be distributed among the beams based on their beam MU. Since this dose value is not related to the BDSPs shown in RayStation, no coordinates or depths will be exported.

If the **IONTRIS** checkbox is checked, the DICOM export will be performed according to the IONTRIS DICOM standard.

6.2 BEAM QUALITY PARAMETERS FOR ION TREATMENT MACHINES

This section describes the beam quality parameters. The beam quality consists of beam model parameters and other parameters that affect the plan creation and dose computation in RayStation. Each Ion treatment machine has at least one beam quality, which is used for dose computation in RayPhysics and, once the machine is commissioned, in RayStation.

The ion beam model parameters for PBS and Line scanning are visible in the following tabs:

Spot profiles, **Pristine Bragg peaks** and **Absolute dosimetry**. The focal length is visible in the **General** tab.

For Uniform Scanning, Double Scattering and Wobbling the beam model parameters are stored in a set of beam models referred to as Range Options. The beam model parameters are not visible in RayPhysics but other properties for each range option are shown.

In this section

This section contains the following sub-sections:

6.2.1	General	p. 275
6.2.2	Range options	p. 278
6.2.3	Scanning data	p. 281
6.2.4	Enter measurements	p. 288
6.2.5	Auto-modeling of proton beam model parameters	p. 291
6.2.6	Spot profile dose curve computation	p. 297
6.2.7	Pristine Bragg peak dose curve computation	p. 299
6.2.8	Absolute dosimetry point dose computation	p. 302

6.2.1 General

This section describes the **General** tab in the Beam quality parameters workspace for Ion treatment machines.

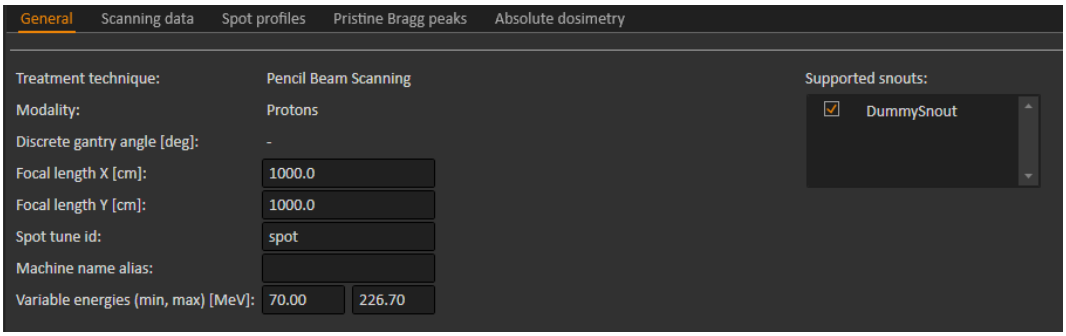


Figure 130. The **General** tab for variable energies.

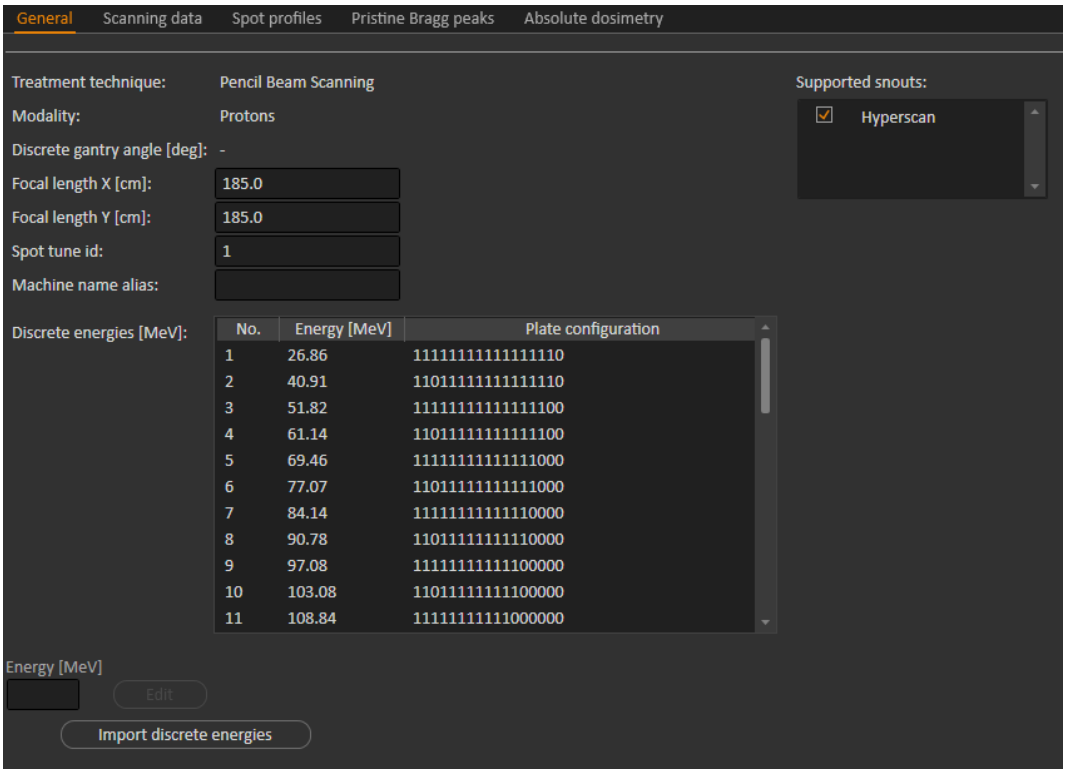


Figure 131. The **General** tab for discrete energies.

Treatment technique

Supported treatment techniques are: Pencil Beam Scanning, Line Scanning, Uniform Scanning, Double Scattering and Wobbling.

Modality

Supported modalities are protons and carbon ions.

Discrete gantry angle [deg]

Only set for machines with a number of fixed gantry angles. Each angle will have a separate beam model for dose computation.

Focal length X, Y [cm]

Effective focal lengths (cm) for X and Y deflection (IEC 61217 gantry coordinate system). Used as the virtual source axis distance to determine the mean direction of the protons and is part of the beam model parameters.

This parameter is only used for PBS, Line Scanning and Uniform Scanning machines. Double Scattering and Wobbling machines use focal length dependent on the energy populated in the beam model.

Spot tune id

Identifier for a given spot (size) configuration. Exported to DICOM in tag Scan Spot Tune ID (300A,0390). Note that it will not be possible to perform automodel or compute dose if the Spot tune id is updated after dose curves have been imported to the machine.

Machine name alias

If a machine name alias is set it will be used during DICOM export to override the machine name. If used in combination with discrete gantry angles, it will allow different machine names for the different beam lines.

Supported energies

Either variable energies (min/max) or a set of discrete energies.

Variable energies

The minimum and maximum supported energy can be specified. All energies in the interval are supported by the machine.

Figure 132. Variable energies.

Discrete energies

For machines with support only for a set of discrete energies, this set is displayed in a table.

To edit the discrete energies table: select a row in the table, enter a new value in the **Energy [MeV]** field and then click **Edit**.

Select to import discrete energies from a text file by clicking the **Import discrete energies** button.

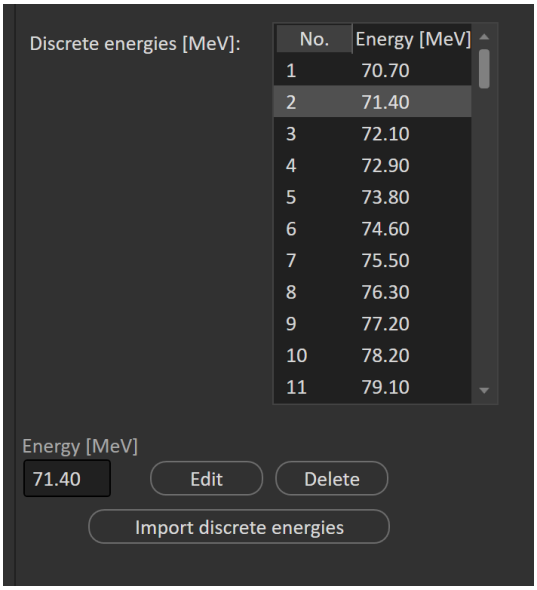


Figure 133. Discrete energies.

Supported snouts

The selected snouts are supported for this beam quality. (For machines with discrete gantry angles it is possible to have different sets of allowed snouts per beam quality.)

6.2.2 Range options

This section describes the **Range Options** tab in the Beam quality parameters workspace for Ion treatment machines (visible for US/DS/Wobbling techniques). The **Range Options** tab contains a list of all range options and their detailed parameters. The beam model is not displayed.

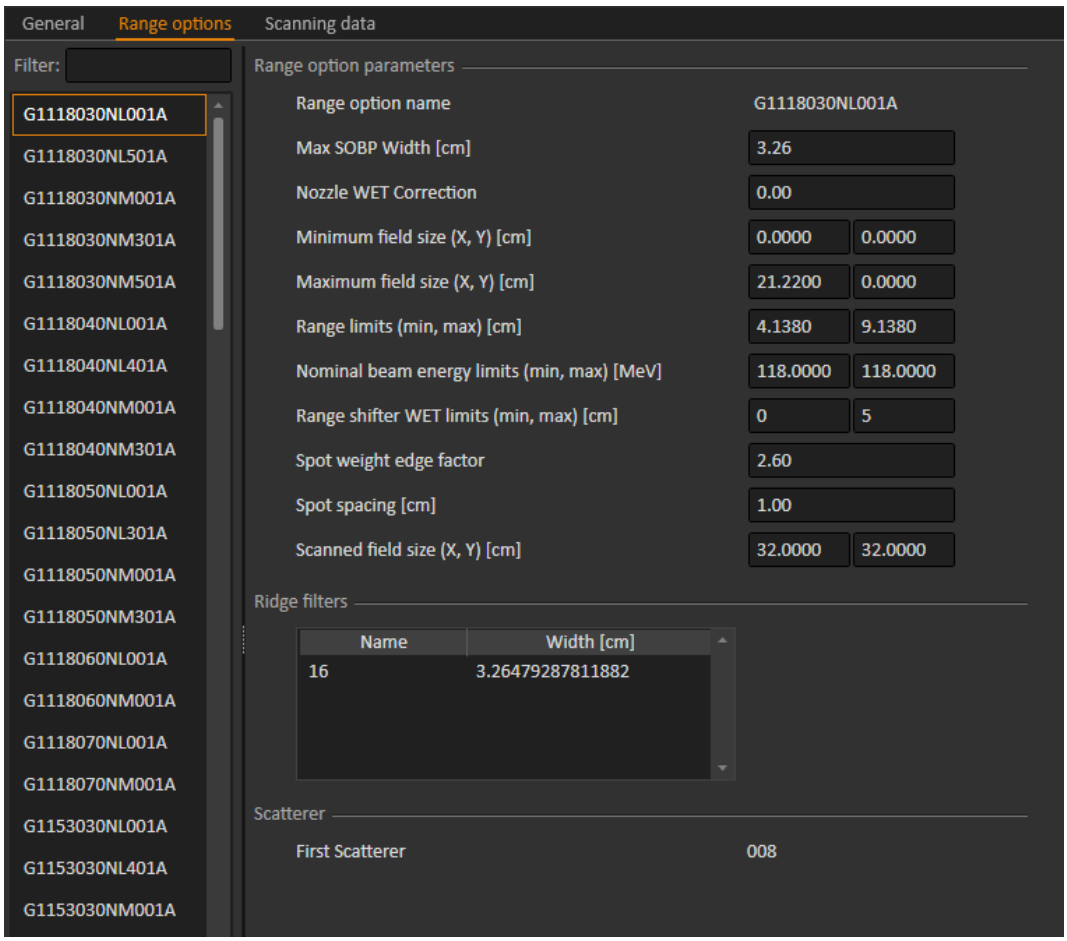


Figure 134. The **Range Options** tab.

Filter

To filter the range options, enter the desired characters in the **Filter** field. To search for a range option by name, enter the name in the **Filter** field.

Range option parameters

The **Range option parameters** list displays the nozzle settings parameters of the selected range option. Each range option also has a set of beam model parameters, which are not yet displayed.

The **Range option name** displays the currently selected range option and cannot be edited. The following parameters can be set for the selected range option:

- **Max SOBP Width [cm]** - The maximum allowed spread out Bragg peak width for the selected range option.
- **Nozzle WET Correction** - Water equivalent thickness correction for the nozzle mounted objects. Should be zero if no correction is needed.
- **Minimum field size (X, Y) [cm]** - The minimum allowed collimated field size at isocenter for the selected range option (IEC 61217 gantry coordinate system). If only the X value is entered, the value is interpreted as the diameter of a circle. If both X and Y values are entered, the values are interpreted as the width and height of a rectangle. The fields shall be left blank if the range options have no field size dependence.
- **Maximum field size (X, Y) [cm]** - The maximum allowed collimated field size at isocenter for the selected range option (IEC 61217 gantry coordinate system). If only the X value is entered, the value is interpreted as the diameter of a circle. If both X and Y values are entered the values are interpreted as the width and height of a rectangle. The fields shall be left blank if the range options have no field size dependence.
- **Range limits (min, max) [cm]** - The minimum and maximum allowed range for the selected range option.
- **Nominal beam energy limits (min, max) [MeV]** - The minimum and maximum allowed nominal beam energies for the selected range option. Can be used instead of, or in combination with, the range limits.
- **Range shifter WET limits (min, max) [cm]** - Only visible for Mitsubishi Electric Co SELECT BEAM NOZZLE in Uniform Scanning mode and if a value has been entered. The minimum and maximum allowed water equivalent thickness of the range shifter for the selected range option.
- **Meterset rate [MU/minute]** or **[NP/minute]** - Only visible for Double Scattering. If a value is entered it will be exported in the first control point in the DICOM ion control points sequence. The displayed unit depends on the machine primary dosimeter unit.

The following three fields are only visible for Mitsubishi Electric Co SELECT BEAM NOZZLE in Uniform Scanning mode. They are used to define a rectangular spot pattern in a regular grid to be used at DICOM export in the ion control points sequence.

- **Spot weight edge factor** - The factor by which the weight of the spots at the edges in the spot pattern shall be multiplied, compared to the weights of the spots in the rest of the spot pattern. Only visible if a value has been entered.
- **Spot spacing [cm]** - The spot spacing to be used in the spot pattern. Only visible if a value has been entered.
- **Scanned field size (X, Y) [cm]** - The size in X and Y direction (IEC 61217 gantry coordinate system) of the rectangular spot pattern.

Ridge filters/range modulators

The section contains a table with the available ridge filters/range modulators for the selected range option. This section is only visible for treatment machines that have ridge filters or range modulators with fixed weights. All ridge filters/range modulators available for the treatment machine are listed in *Range modulators/Ridge filters on page 257*. The **Name** and **Width [cm]** of each ridge filter/range modulator is displayed in the table.

Scatterer

This section shows the first scatterer and if applicable the second scatter (only for Double Scattering) for the selected range option. All the available scatteres for the machine is listed in *Scatterers on page 257*.

6.2.3 Scanning data

This section describes the **Scanning data** tab in the Beam quality parameters workspace for Ion treatment machines.

Default planning parameters

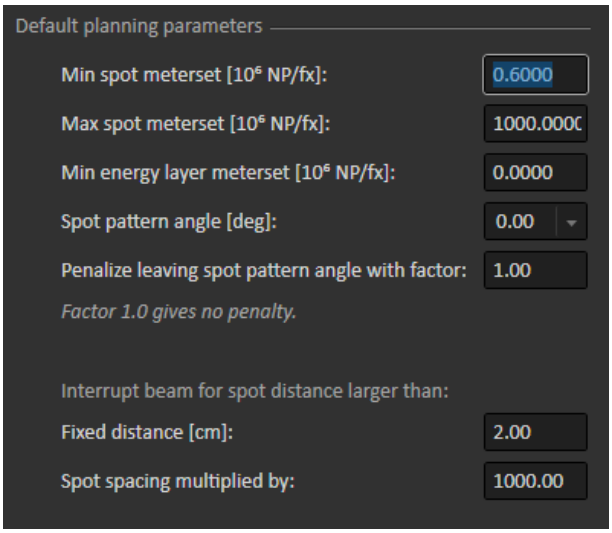


Figure 135. The default planning parameters in the **Scanning data** tab.

The default planning parameters are machine limits used to create a deliverable plan. Some of the parameters can be overridden in the Plan Optimization module in RayStation (see *RSL-D-RS-9A-USM, RayStation 9A User Manual* for more information).

- **Min spot meterset** [MU/fx] or [10^6 NP/fx] is the default minimum meterset for a spot used in spot filtering and spot weight bounding during optimization. The unit depends on the primary dosimeter unit of the machine. Min spot meterset has unit [MU/fx per cm] for Line Scanning. This parameter can be overridden in RayStation.
- **Max spot meterset** [MU/fx] or [10^6 NP/fx] is the maximum meterset for a spot used in spot weight bounding during optimization. The unit depends on the primary dosimeter unit of the machine. The max spot meterset is applied as an upper bound from the first iteration. If set to 0, no bounds will be applied during optimization. N/A for Line Scanning.
- **Min energy layer meterset** [MU/fx] or [10^6 NP/fx] is the minimum meterset for an energy layer used in energy layer filtering and energy layer meterset bounding during optimization. The unit depends on the primary dosimeter unit of the machine.
- **Spot pattern angle [deg]** is the default value used when the spot pattern is initialized when starting an optimization and when sorting spots. This parameter can be overridden in RayStation. For more information, refer to the *RSL-D-RS-9A-USM, RayStation 9A User Manual*.

- **Penalize leaving fast direction with factor** is the default factor by which distances to spots that leave the fast direction are multiplied when sorting the spots. This is used if spot sorting is selected, refer to the *RSL-D-RS-9A-USM, RayStation 9A User Manual* for more information. This parameter can be overridden in RayStation.
- **Beam interruption settings** contains default values and they are only applicable for quasi-discrete machines. The positions between which to interrupt the beam are determined by two parameters: a **Fixed distance** and the **Spot spacing multiplied by a factor**. For all distances larger than the smaller of these two values, the beam will be turned off. For information about quasi-discrete optimization settings, refer to the *RSL-D-RS-9A-USM, RayStation 9A User Manual*. These parameters can be overridden in RayStation.

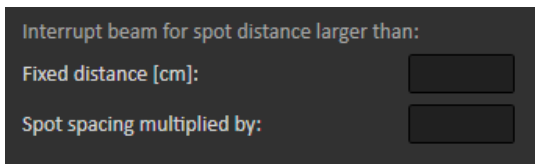


Figure 136. The **Beam interruption** settings (only applicable for quasi-discrete machines).

Meterset rate parameters

The following properties are visible in the Meterset rate parameters section:

- **Meterset rate [MU/minute]** is only used in DICOM export and not in RayStation. If this value is set, it is DICOM exported in the Meterset Rate (300A,035A) tag in the first control point in the Ion Control Point Sequence. This parameter is only visible for machines that do not have an energy dependent meterset rate table.

Meterset rate parameters for Line Scanning

The following properties are visible in the Meterset rate parameters section for Line Scanning:

- A Meterset rate table with minimum and maximum Meterset rate limits [MU/s] for an energy interval [MeV].

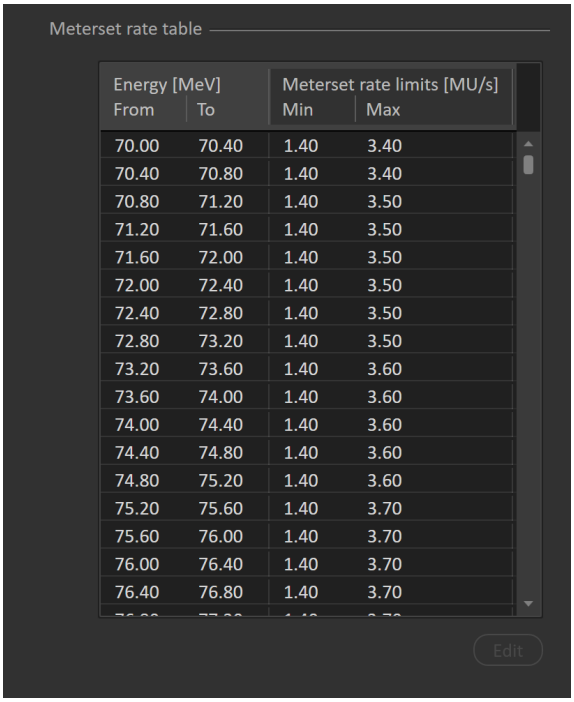


Figure 137. The **Meterset rate settings** for Line Scanning.

Meterset rate parameters for Mitsubishi Electric Co PBS

The following properties are visible in the Meterset rate parameters section for Mitsubishi Electric Co PBS:

- **Setting ID** - Name of the set of Meterset rates.
- A Meterset rate table with Meterset rate [MU/minute] for each energy [MeV] for the selected Setting ID.

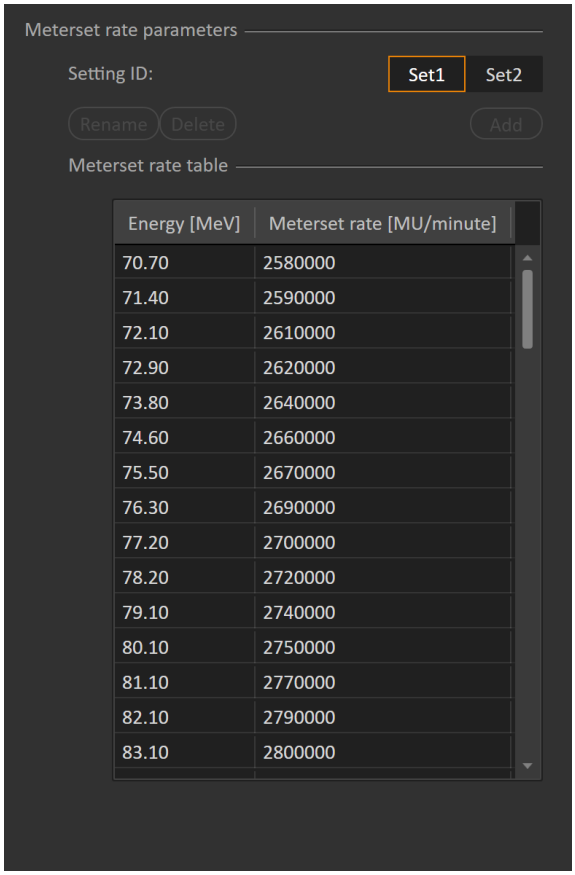


Figure 138. The **Meterset rate settings** for a Mitsubishi Electric Co PBS.

Meterset rate parameters for Mitsubishi Electric Co US

For Mitsubishi Electric Co Uniform Scanning machines, only the meterset rate settings table is visible in the **Scanning data** tab. It is also possible to specify a value for **Minimum fraction dose** in the beam dose specification point for each setting. The dose unit will depend on the dose type set for the treatment machine, PHY or RBE.

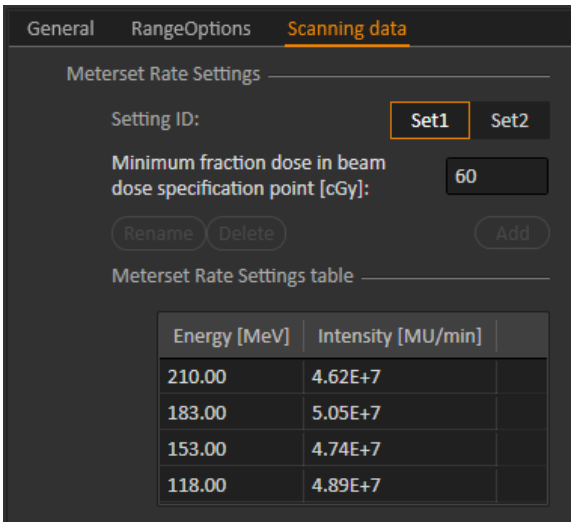


Figure 139. The **Meterset rate settings** for a Mitsubishi Electric Co SELECT BEAM NOZZLE in Uniform Scanning mode. The dose unit will depend on the dose type set for the treatment machine, PHY or RBE.

Beam scanning parameters for Line Scanning and quasi-discrete PBS

The following properties are visible in the Beam scanning parameters section for Line Scanning and quasi discrete PBS:

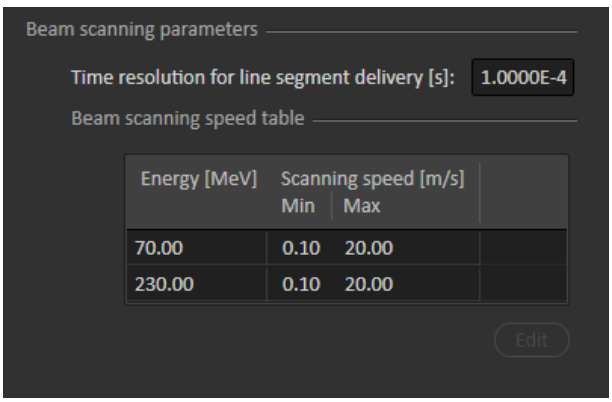


Figure 140. The Beam scanning parameters for Line Scanning.

- **Time resolution for line segment delivery [s]** is the smallest time resolution in seconds for scanning a line segment in Line Scanning. Only visible for Line Scanning machines.
- **Minimum time per spot [s]** is the smallest time resolution in seconds for delivering a spot in quasi-discrete PBS. This parameter is only visible for certain machine configurations.

- A Beam scanning speed table describing minimum and maximum scanning speeds [m/s] per energy [MeV]. Maximum scanning speed set to zero means that the minimum and maximum values are equal, i.e., the scanning speed is constant.

Beam scanning parameters for Mitsubishi Electric Co machines

The following parameters are possible to specify in the beam scanning parameters section for for Mitsubishi Electric Co. PBS machines:

- **Control time [s]** - the amount of time taken before and after a scan, for example, the time taken to issue an instruction to start the scan.
- **Response time [s]** - the minimum amount of time for a scan
- a **Beam scanning speed table** with scanning speeds [m/s] in X and Y direction (IEC 61217 gantry coordinate system)

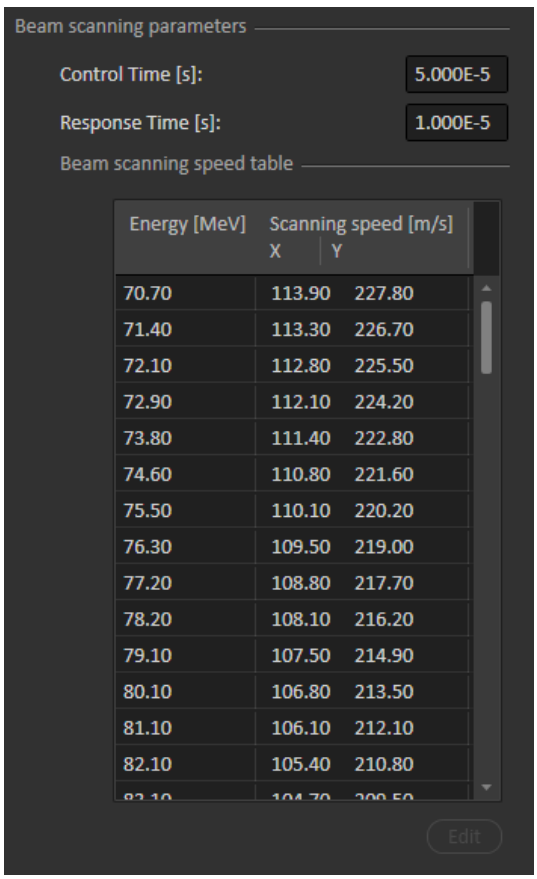


Figure 141. The **Beam scanning parameters** for a Mitsubishi Electric Co SELECT BEAM NOZZLE in PBS mode.

Synchrotron parameters

These parameters are used for setting the intensity of each energy layer and are only applicable for synchrotrons. The spill length is the duration of a beam extraction in seconds and the number of particles per spill are the number of particles that are extracted during a spill. A degrader value can be added to reduce the beam current. The degrader value is in the range 0 to 1, where 0 corresponds to no degradation and 1 to full degradation.

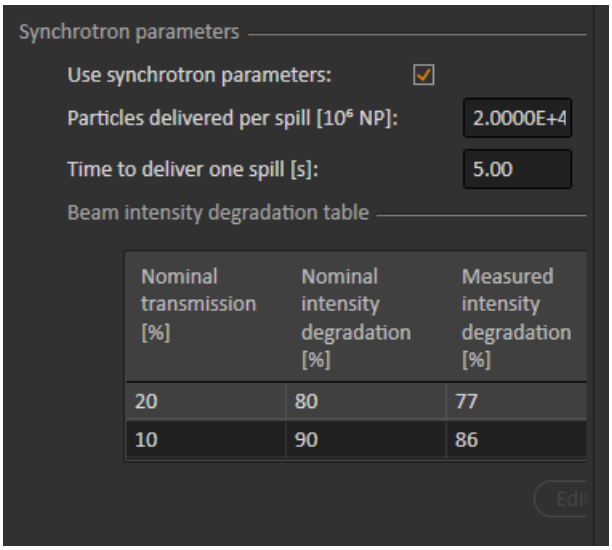


Figure 142. The **Synchrotron parameters** for a synchrotron machine.

6.2.4 Enter measurements

This section describes how measurements are imported, exported or deleted into/from the RayPhysics system.

In this section

This section contains the following sub-sections:

6.2.4.1	Import curves	p. 288
6.2.4.2	Export curves	p. 288
6.2.4.3	Remove curves	p. 289

Import curves

To import dose curves measured to the selected machine and beam quality, click the **Import curves** button. For ion machines only the file format *.csv is supported. It can be opened, reviewed and edited in a text editor. The file format is described in detail in *section B.2.5 Ion treatment machines on page 386* and the required beam data is described in the *RSL-D-RS-9A-BCDS, RayStation 9A Beam Commissioning Data Specification*.

If you are working in the **Spot profiles** tab, only spot profile dose curves can be imported when clicking the **Import curves...** button. Similarly, when working in the **Pristine Bragg peaks** tab or the **Absolute dosimetry** tab, only the corresponding dose curves can be imported.

Note: *For Ion treatment machines, all negative values in depth dose curves are set to 0 during import.*

WARNING!

Always review curves after import. Always review curves after import to ensure consistency with the measurement situation. The beam model quality depends critically on correctness of the imported data. (508984)

Export curves

All measured and computed curves for a selected treatment machine and beam quality can be exported to the .csv format.

To export all curves for a selected beam quality:

1. Click the **Export curves** button to open a dialog showing all dose curves that can be exported.

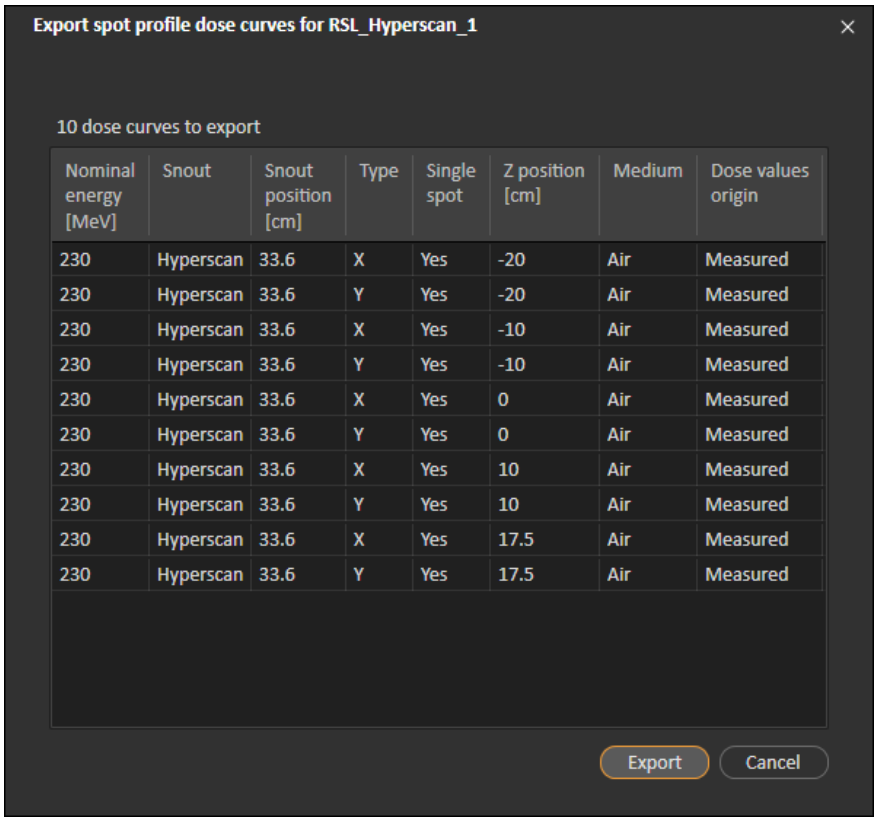

Export spot profile dose curves for RSL_Hyperscan_1
10 dose curves to export
Nominal energy [MeV]
Snout
Snout position [cm]
Type
Single spot
Z position [cm]
Medium
Dose values origin
230 Hyperscan 33.6 X Yes -20 Air Measured
230 Hyperscan 33.6 Y Yes -20 Air Measured
230 Hyperscan 33.6 X Yes -10 Air Measured
230 Hyperscan 33.6 Y Yes -10 Air Measured
230 Hyperscan 33.6 X Yes 0 Air Measured
230 Hyperscan 33.6 Y Yes 0 Air Measured
230 Hyperscan 33.6 X Yes 10 Air Measured
230 Hyperscan 33.6 Y Yes 10 Air Measured
230 Hyperscan 33.6 X Yes 17.5 Air Measured
230 Hyperscan 33.6 Y Yes 17.5 Air Measured
Export
Cancel

Figure 143. The Export spot profile dose curves dialog.

2. Select **Export** to export the curves. This opens the Browse for folder dialog.
3. Specify a location for the exported dose curves.
4. Click **OK**.

If you are working in the **Spot profiles** tab, spot profile dose curves will be exported when clicking the **Export curves...** button. Similarly, when working in the **Pristine Bragg peaks** tab or **Absolute dosimetry** tab, the corresponding dose curves can be exported.

Remove curves

To remove dose curves for a selected treatment machine and beam quality:

1. Click the **Remove curves...** button.

   This opens the Remove curves dialog.

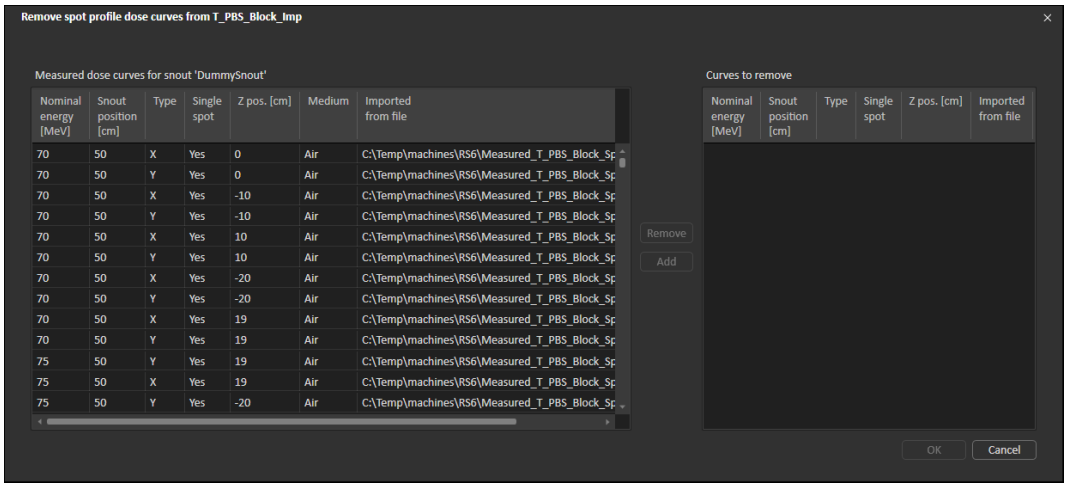

Remove spot profile dose curves from T_PBS_Block_Imp
Measured dose curves for snout 'DummySnout'
Nominal energy [MeV]
Snout position [cm]
Type
Single spot
Z pos. [cm]
Medium
Imported from file
70 50 X Yes 0 Air C:\Temp\machines\RS6\Measured_T_PBS_Block_Sp
70 50 Y Yes 0 Air C:\Temp\machines\RS6\Measured_T_PBS_Block_Sp
70 50 X Yes -10 Air C:\Temp\machines\RS6\Measured_T_PBS_Block_Sp
70 50 Y Yes -10 Air C:\Temp\machines\RS6\Measured_T_PBS_Block_Sp
70 50 X Yes 10 Air C:\Temp\machines\RS6\Measured_T_PBS_Block_Sp
70 50 Y Yes 10 Air C:\Temp\machines\RS6\Measured_T_PBS_Block_Sp
70 50 X Yes -20 Air C:\Temp\machines\RS6\Measured_T_PBS_Block_Sp
70 50 Y Yes -20 Air C:\Temp\machines\RS6\Measured_T_PBS_Block_Sp
70 50 X Yes 19 Air C:\Temp\machines\RS6\Measured_T_PBS_Block_Sp
70 50 Y Yes 19 Air C:\Temp\machines\RS6\Measured_T_PBS_Block_Sp
75 50 Y Yes 19 Air C:\Temp\machines\RS6\Measured_T_PBS_Block_Sp
75 50 X Yes 19 Air C:\Temp\machines\RS6\Measured_T_PBS_Block_Sp
75 50 Y Yes -20 Air C:\Temp\machines\RS6\Measured_T_PBS_Block_Sp
Remove
Add
Curves to remove
Nominal energy [MeV]
Snout position [cm]
Type
Single spot
Z pos. [cm]
Imported from file
OK
Cancel

Figure 144. The Remove spot profile dose curves dialog.

2. Select a curve in the list and click the **Remove** button.
3. Click **OK**.

If you are working in the **Spot profiles** tab, spot profile dose curves will be removed when clicking the **Remove curves...** button. Similarly, when working in the **Pristine Bragg peaks** tab or **Absolute dosimetry** tab, the corresponding dose curves can be removed.

6.2.5 Auto-modeling of proton beam model parameters

This section describes the auto-modeling of proton beam model parameters. Automodeling is not supported for Mevion Hyperscan machines, carbon ion machines and US/DS/wobbling machines.

In this section

This section contains the following sub-sections:

6.2.5.1	Launch auto-modeling	p. 291
6.2.5.2	Prerequisites for auto-modeling	p. 291
6.2.5.3	Auto-modeling of spot profiles	p. 292
6.2.5.4	Auto-modeling of pristine Bragg peaks	p. 293
6.2.5.5	Auto-modeling of absolute dosimetry	p. 295

Launch auto-modeling

Auto-modeling can be launched from the beam model parameters workspace by clicking the **Auto model** button in the top bar when working in any of the beam model parameter tabs. The treatment machine must be in edit mode.

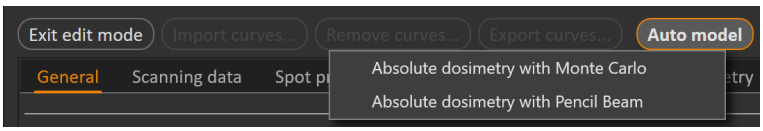


Figure 145. The **Auto model** button in the top bar.

There are two auto-modeling options, which determines what dose engine to use for the absolute dosimetry calculation step in the auto-modeling:

- Absolute dosimetry with Monte Carlo
- Absolute dosimetry with Pencil Beam

The auto-modeling consists of three steps, which are performed automatically after each other:

- Modeling of spot profiles
- Modeling of pristine Bragg peaks
- Modeling of absolute dosimetry

Prerequisites for auto-modeling

All machine geometry parameters must be correctly filled out and dose curves must be imported before the auto-modeling procedure can start. The energies of the spot profile and pristine Bragg peak measurements must cover the minimum and maximum energy supported by the machine. The minimum and maximum energy for the measured absolute dosimetry must exactly match the

minimum and maximum energy supported by the machine. For further details, refer to the *RSL-D-RS-9A-BCDS, RayStation 9A Beam Commissioning Data Specification*. Furthermore, for each energy there must exist spot profiles in both X and Y directions for at least three different depths, covering the range of therapeutic interest.

Note: *Auto-modeling is not yet supported for machines with an energy selector (Mevion Hyperscan).*

Auto-modeling of spot profiles

The auto-modeling of spot profiles consists of the following steps:

1. Each spot profile is first fitted by a single Gaussian profile using a least-square fit.
2. The standard deviation, $\sqrt{\overline{r_0^2}}$, is extracted from each fitted Gaussian profile.
3. For each energy, the standard deviations at different depths (IEC 61217 Machine coordinate systems), z, are fitted to the Fermi-Eyges transport equation (refer to the *RSL-D-RS-9A-REF, RayStation 9A Reference Manual* for more details):

$$\overline{r^2}(z) = \overline{r^2}(0) + 2\overline{r\theta}(0)\ z + \overline{\theta^2}(0)\ z^2$$

Resulting beam model parameters for spot profiles

The result of the fit is the set of spatial angular moments or Fermi Eyges parameters, $\overline{\theta^2}$ (angular variance or spread), $\overline{r\theta}$ (spatial-angular covariance or divergence), $\overline{r^2}$ (spatial variance or spot size at isocenter), for each energy.

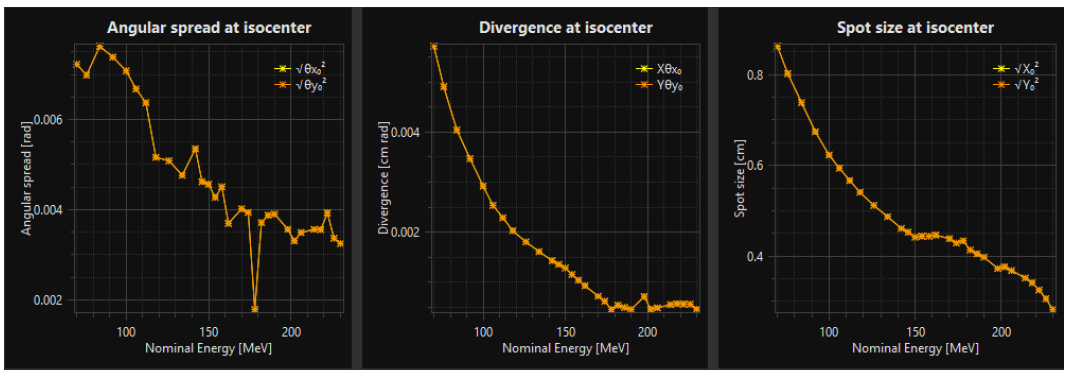


Figure 146. The beam model parameter graphs for Spot profiles.

Nominal Energy [MeV]	Angular spread [rad] $\sqrt{\theta x_0^2}$	$\sqrt{\theta y_0^2}$	Divergence [cm rad] $X\theta x_0$	$Y\theta y_0$	Spot size [cm] $\sqrt{X_0^2}$	$\sqrt{Y_0^2}$
70.00	0.00772	0.00772	0.00238	0.00238	0.674	0.674
75.00	0.00693	0.00693	0.00217	0.00217	0.628	0.628
80.00	0.00624	0.00624	0.00194	0.00194	0.597	0.597
85.00	0.0061	0.0061	0.00161	0.00161	0.57	0.57
90.00	0.00556	0.00556	0.00143	0.00143	0.551	0.551
95.00	0.006	0.006	0.00131	0.00131	0.521	0.521
100.00	0.00464	0.00464	0.00129	0.00129	0.499	0.499
105.00	0.00465	0.00465	0.00117	0.00117	0.484	0.484
110.00	0.00434	0.00434	0.00114	0.00114	0.459	0.459
115.00	0.00466	0.00466	0.00106	0.00106	0.448	0.448
120.00	0.00425	0.00425	0.000952	0.000952	0.434	0.434
125.00	0.00287	0.00287	0.000787	0.000787	0.42	0.42

Figure 147. The beam model parameter table for Spot profiles.

After the auto-modeling is complete the spatial angular moments for each energy at the isocenter $\overline{\theta^2}$ $\overline{r\theta_{0_2}}$ $\overline{r_0^2}$ are shown in the table and graphs in the **Spot profiles** tab in the Beam model parameters workspace. For more information of how the spatial angular moments are used in the RayStation dose computation, refer to the *RSL-D-RS-9A-REF, RayStation 9A Reference Manual* (Proton dose computation).

Note: *The auto-model process will generate beam model parameters that are equal in X and Y (IEC 61217 gantry coordinate system). If the measured spot profiles differ significantly in X and Y, i.e. the spot shape is elliptical and not circular, please contact RaySearch support for advice.*

Note: *The measured spot profiles are fitted to a single Gaussian profile. If the measured spot profiles differs significantly from a single Gaussian and might be better represented by a double Gaussian, please contact RaySearch support for advice.*

Validation of the beam model parameters for spot profiles

Divergence [cm rad] - $\overline{r\theta}$ should be positive for a divergent beam.

Spot size [cm] - $\sqrt{\overline{r^2}}$ should be in the order of millimeters.

Auto-modeling of pristine Bragg peaks

In the auto-modeling of pristine Bragg peaks, a linear combination of pre-computed mono-energetic pristine Bragg peaks is fitted to the measured pristine Bragg peak for each nominal energy. This generates an energy spectrum. The pre-computed Bragg peaks have been computed with the

RayStation Monte Carlo dose engine, and integrated laterally using a circular detector with a diameter of 8.16 cm, 11.0 cm or 12.0 cm. The suitable set of pre-computed Bragg peaks are automatically selected according to the registered detector width of the measured curves during auto-modeling. For single spot measurements, only detector sizes with diameter 8.16 cm and 12.0 cm are supported. For scanned fields, a virtual circular detector of diameter 11.0 cm is used. It is possible to view and edit the detector information in the **Measurement conditions** dialog, see *Measurement conditions on page 301*.

Resulting beam model parameters for pristine Bragg peaks

The result of the auto-modeling of pristine Bragg peaks is an energy spectrum, with an energy histogram for each nominal energy, where each bin value corresponds to a weight of the corresponding pre-computed mono-energetic pristine Bragg peak. The energy spectrum graph is displayed in the upper part of the **Pristine Bragg peaks** tab in the Beam model parameters workspace.

The R80 Energy table and graph corresponds to the energy of the pre-calculated mono-energetic pristine Bragg peak giving the same R80 range as the depth dose curve generated from the corresponding energy histogram. For more information on how the energy spectra are used in the RayStation dose computation, refer to the *RSL-D-RS-9A-REF, RayStation 9A Reference Manual* (Proton dose computation).

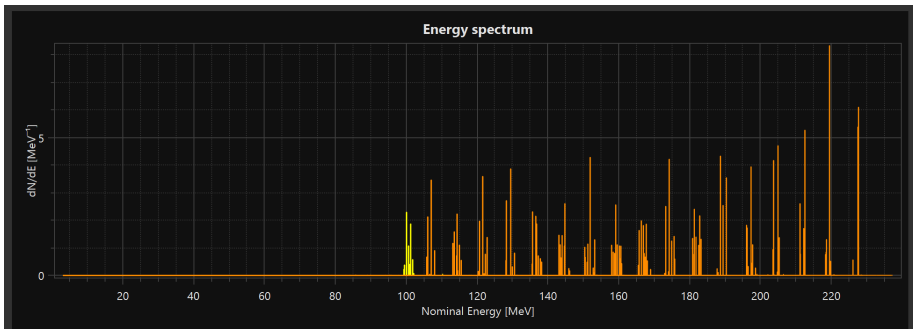


Figure 148. The beam model parameter graph for pristine Bragg peaks.

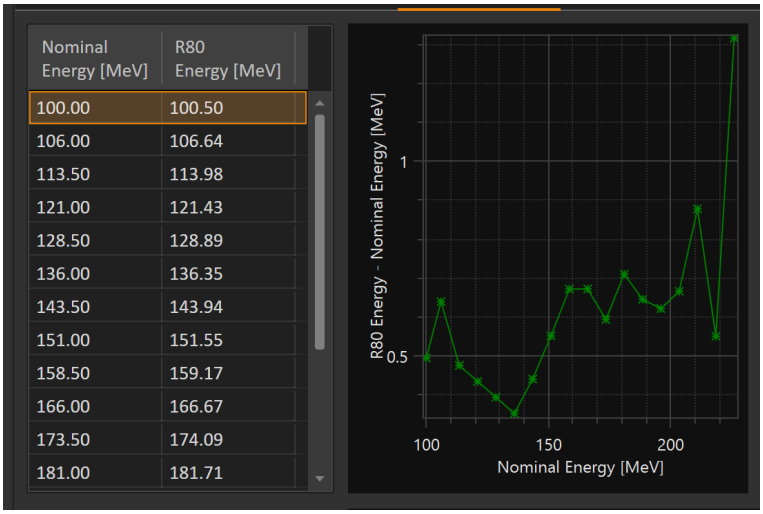


Figure 149. The R80 Energy table and graph for pristine Bragg peaks.

Validation of beam model parameters for pristine Bragg peaks

Go through the energy spectra by filtering on energy:

- The energy spectra should be clean and bins positioned around the corresponding energy.
- Bins that appear towards lower energies can be an indication that a scanned field has been modeled as a single spot measurement.

Auto-modeling of absolute dosimetry

The auto-modeling of absolute dosimetry is performed by a forward dose calculation for the selected dose engine with the selected dose computation parameters and measurements conditions using an initial value for the beam meterset calibration. During the dose computation, the computed dose is averaged over the dose detector area. The beam meterset calibration for each nominal energy is subsequently scaled, so that the computed dose at the measurement depth equals the measured dose. Recommended number of histories is at least 50,000, when performing the auto-modeling with Monte Carlo. If the machine is to be commissioned both for Pencil Beam and Monte Carlo, it is strongly recommended to auto-model the machine with Monte Carlo for the absolute dosimetry.

Resulting beam model parameters for Absolute dosimetry

The result of the auto-modeling is the beam meterset calibration as a function of energy. It is displayed in a table and graph in the **Absolute dosimetry** tab in the Beam model parameters workspace. The beam meterset calibration is given in Ions per MU or NP, depending on the machine primary dosimeter unit. The beam meterset calibration relates to the number of ions to be used in the Monte Carlo dose computation or to the scale factor to be used for the pre-computed pristine Bragg peaks in the Pencil beam dose computation. For more information on how the beam meterset calibration is used in the RayStation dose computation, refer to the *RSL-D-RS-9A-REF, RayStation 9A Reference Manual* (Proton dose computation).

The table with Ions per MU or NP is editable, if the absolute dosimetry of the beam model needs to be scaled after the auto-modeling is completed.

Nominal Energy [MeV]	Beam meterset calibration Ions per MU
100.00	6.961E+7
106.00	7.291E+7
113.50	7.562E+7
121.00	7.854E+7
128.50	8.394E+7
136.00	8.710E+7
143.50	9.070E+7
151.00	9.470E+7
158.50	9.788E+7
166.00	1.008E+8
173.50	1.038E+8
181.00	1.065E+8

Figure 150. The beam model parameter table for Absolute dosimetry.

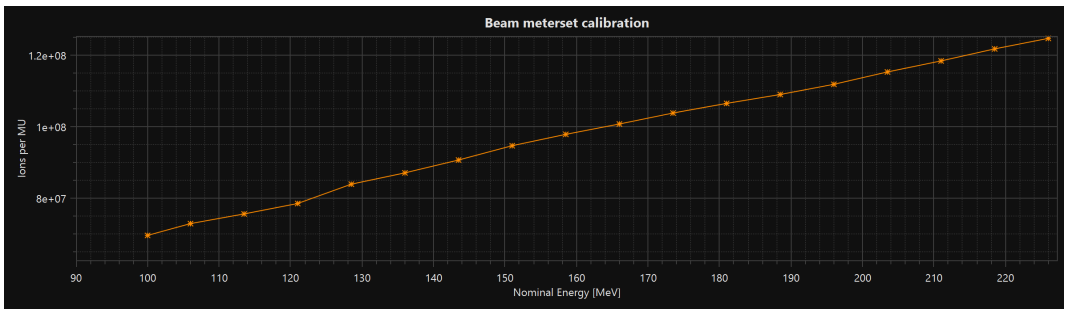


Figure 151. The beam model parameter graph for Absolute dosimetry.

Validation of beam model parameters for absolute dosimetry

The Beam meterset calibration curve shall be smooth. If there are kinks on the curve, it is likely that a measurement is bad or that a too high statistical uncertainty has been used (for Monte Carlo).

6.2.6 Spot profile dose curve computation

This section describes the dose curve computation in the **Spot profiles** tab in the Beam quality parameters workspace for Ion treatment machines, where it is possible to compare all measured and computed spot profiles based on the beam model parameters. The beam model parameters are described in further detail in *section 6.2.5 Auto-modeling of proton beam model parameters on page 291*.

It is also possible to import, export or remove measured and/or computed spot profiles to/from RayPhysics. For more information, see *section 6.2.4 Enter measurements on page 288*.

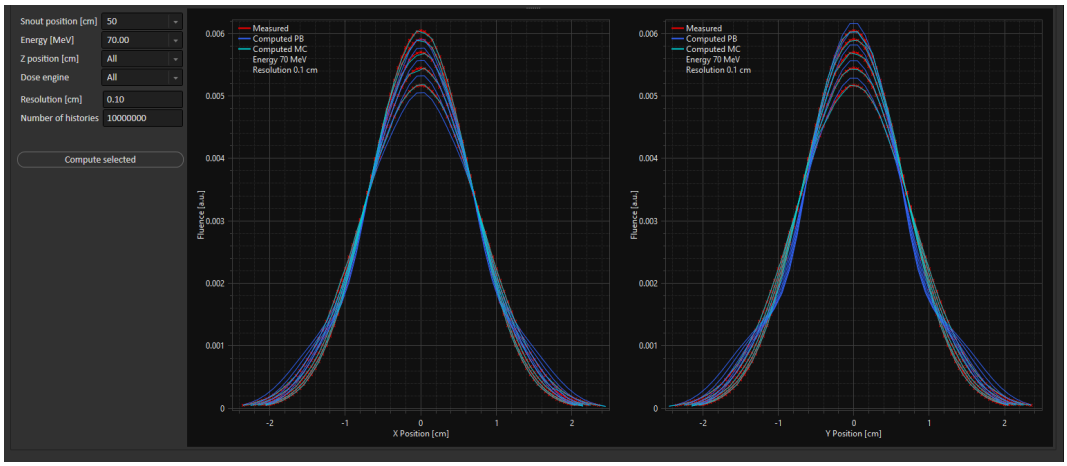


Figure 152. The measured and computed curves in the **Spot profiles** tab.

Filter curves

The curves can be filtered based on the following parameters:

- **Snout position**: It is possible to view all curves or curves measured for a single snout position.
- **Energy**: It is possible to view all curves or curves measured for a single energy.
- **Depth**: It is possible to view all curves for all depths or a single depth.
- **Dose engine**: It is possible to view curves computed by either the Pencil Beam or the Monte Carlo dose engine, or by both engines.

Compute curves

Select to compute curves based on the filtered measurements:

- **Compute selected**: Compute curves for the filtered measurements with the selected dose computation parameters.

Note: *When computing curves (dose values) for Mevion Hyperscan, the current machine settings for the energy selector plates and nozzle exit window are used. The system does not recognize if a particular measurement has been taken under different conditions, for example without the nozzle exit window in place. Also note that previously computed curves (dose values) are not invalidated when modifying the energy selector and nozzle exit window machine settings in RayPhysics, but must be manually recomputed to be updated.*

Dose computation parameters

Resolution: Dose grid resolution used/to be used when computing spot profiles. The recommended resolution for validation of the beam model is 0.1 cm.

Number of histories: The number of histories to be used when computing dose with the Monte Carlo dose engine. Recommended number of histories is at least 10,000,000, however this number can vary from machine to machine.

Note: *The measured curves are not adjusted to be centered around position (0, 0), while the computed curves always are centered around (0, 0). If there is a shift in the measured curves, the measured and computed curves will therefore always be laterally shifted relative to each other.*

Note: *For spot profiles computed with the Pencil Beam dose engine, the following can be observed:*

1. *The computed profiles are not symmetric in the X and Y direction, even though the spatial-angular moments are the same in both directions.*
2. *The computed profiles are not smooth Gaussians, but show some minor discontinuities.*

Both these effects are due to the sub-spot representation, described in detail in the RSL-D-RS-9A-REF, RayStation 9A Reference Manual.

Results from dose computation

The results from the dose computation are displayed in two graphs showing the computed spot profiles in relation to the measured spot profiles in X- and Y-direction (IEC 61217 gantry coordinate system). The displayed computed fluence is extracted from a dose computation in an air phantom. The 3D dose in the air phantom is converted to a point dose, by interpolation at the voxel center coordinates. It is possible to view the result in a logarithmic scale by right-clicking in the graph. Each pair of computed curves is normalized, using the same factor for the X- and Y-curve, to the product of the integrals of the corresponding measured curves.

6.2.7 Pristine Bragg peak dose curve computation

This section describes the dose curve computation in the **Pristine Bragg peaks** tab in the Beam quality parameters workspace for treatment machines, where it is possible to compare all measured and computed Pristine Bragg peaks based on the beam model parameters. The beam model parameters are described in further detail in *section 6.2.5 Auto-modeling of proton beam model parameters on page 291*.

It is also possible to import, export or remove measured and/or computed curves to/from RayPhysics 9A. For more information, see Enter measurements.

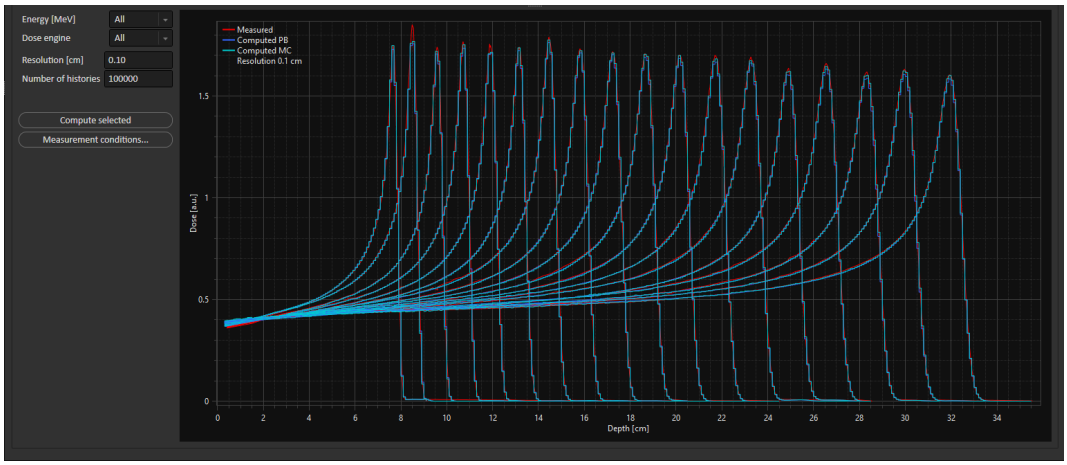


Figure 153. The measured and computed curves in the **Pristine Bragg peaks** tab.

Filter curves

The curves can be filtered based on the following parameters:

- **Energy**: It is possible to view all curves or curves measured for a single energy.
- **Dose engine**: It is possible to view all curves for all dose engines or to select to view curves computed by either the Pencil Beam or the Monte Carlo dose engine.

Compute curves

Select to compute curves based on the filtered measurements:

- **Compute selected**: Compute curves for the filtered measurements with the selected dose computation parameters.

Note: *When computing curves (dose values) for Mevion Hyperscan, the current machine settings for the energy selector plates and nozzle exit window are used. The system does not recognize if a particular measurement has been taken under different conditions, for example without the nozzle exit window in place. Also note that previously computed curves (dose values) are not invalidated when modifying the energy selector and nozzle exit window machine settings in RayPhysics, but must be manually recomputed to be updated.*

Dose computation parameters

Resolution: Dose grid resolution used/to be used when computing pristine Bragg peaks. Recommended resolution for validation of the beam model is 0.1 cm.

Number of histories: The number of histories to be used when computing dose with the Monte Carlo dose engine. Recommended number of histories is at least 400,000 for single spot measurements, however this number can vary from machine to machine. For pristine Bragg peaks measurement based on a scanned field, the number of histories needed is significantly lower.

Measurement conditions

Click the **Measurement conditions...** button to open the corresponding dialog.

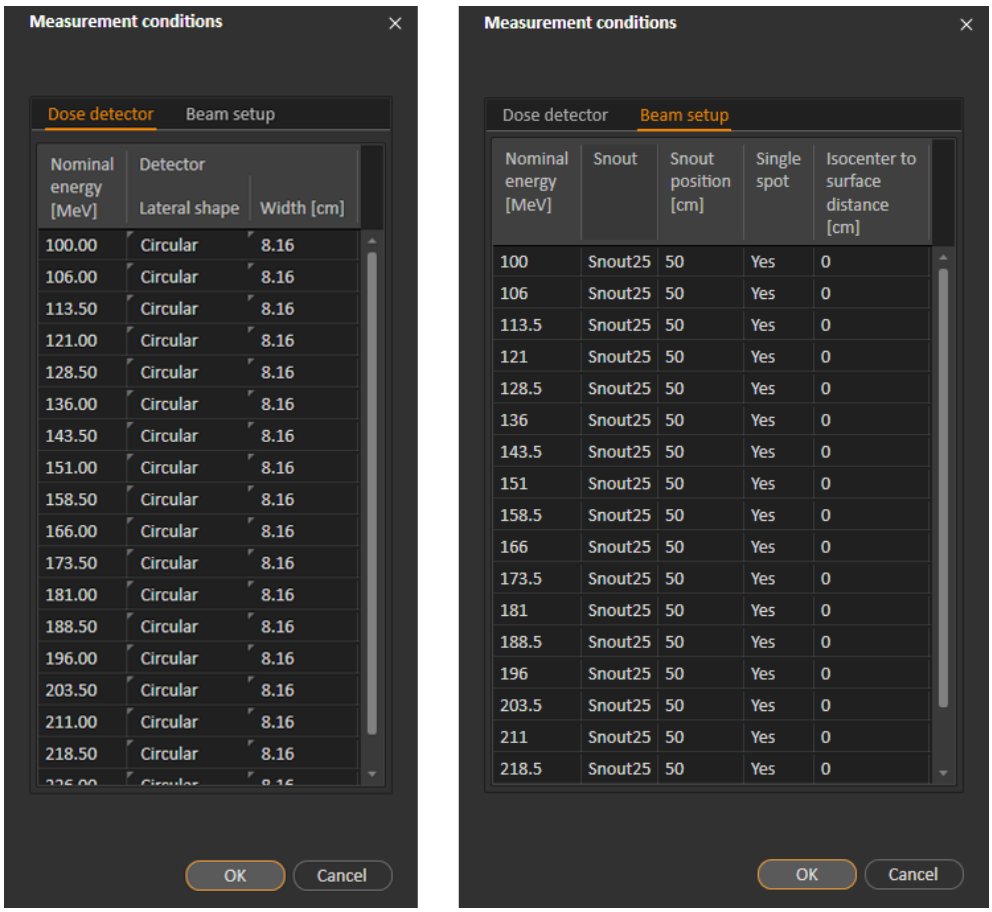


Figure 154. In the **Measurement conditions** dialog it is possible to view beam setup information as well as to view and edit the detector information.

Results from the dose computation

The results from the dose computation is displayed in a graph showing the computed Bragg peak in relation to the measured Bragg peak in the depth direction (Z in the IEC 61217 gantry coordinate system). The displayed computed dose is extracted from the 3D dose distribution at the voxel center coordinates including integration over the detector area. It is possible to toggle to linear interpolated dose by right-clicking in the graph. The computed curves are normalized to the integral of the corresponding measured curve.

6.2.8 Absolute dosimetry point dose computation

This section describes the point dose computation in the **Absolute dosimetry** tab in the Beam quality parameters workspace for Ion treatment machines, where it is possible to compare measured and computed absolute doses based on the beam model parameters. The beam model parameters are described in further detail in *section 6.2.5 Auto-modeling of proton beam model parameters on page 291*.

It is also possible to import, export or remove measured and/or computed point doses to/from RayPhysics 9A. For more information, see Enter measurements.

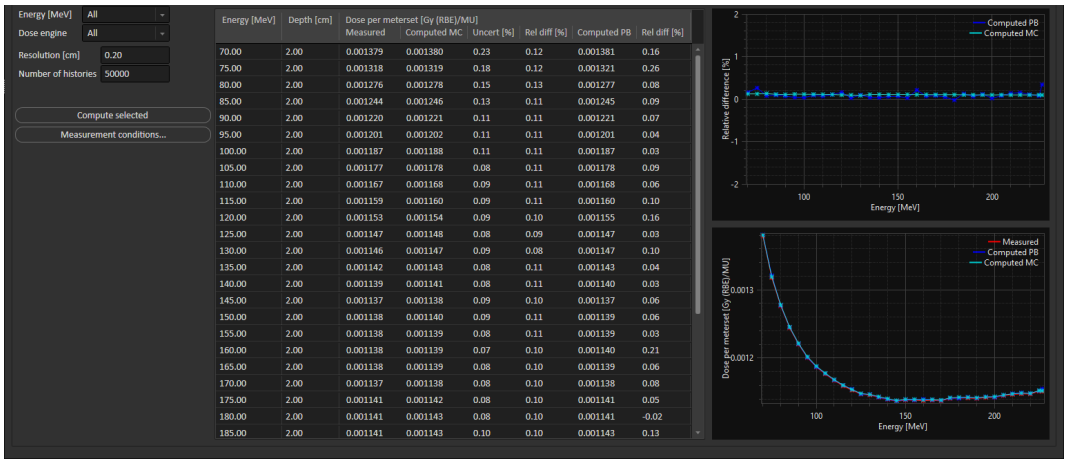


Figure 155. The measured and computed point doses in the **Absolute dosimetry** tab.

Filter curves

The absolute doses can be filtered based on the following parameters:

- **Energy**: It is possible to select to view all absolute doses or absolute dose measured for a specified energy.
- **Dose engine**: It is possible to view the absolute doses for all dose engines or to select to view the absolute doses for either the Pencil Beam or the Monte Carlo dose engine.

Compute doses

Select to compute absolute doses based on the filtered measurements:

- **Compute selected**: Compute absolute doses for the filtered measurements with the selected dose computation parameters.

Note: *When computing curves (dose values) for Mevion Hyperscan, the current machine settings for the energy selector plates and nozzle exit window are used. The system does not recognize if a particular measurement has been taken under different conditions, for example without the nozzle exit window in place. Also note that previously computed curves (dose values) are not invalidated when modifying the energy selector and nozzle exit window machine settings in RayPhysics, but must be manually recomputed to be updated.*

Dose computation parameters

- **Resolution**: Dose grid resolution used/to be used when computing absolute dosimetry. The recommended resolution for validation of the beam model is 0.2 cm.
- **Number of histories**: The number of histories to be used when computing Monte Carlo dose. Recommended number of histories is at least 50,000, however this number can vary from machine to machine.

Measurement conditions

Click the **Measurement conditions...** button to open the corresponding dialog. Note that the detector dimensions for Absolute dosimetry does not have to correspond to the physical dimensions of the

detector used for measurements, since the detector dimensions will only be used to decrease effects of local fluctuations in the Monte Carlo dose computation, as described below.

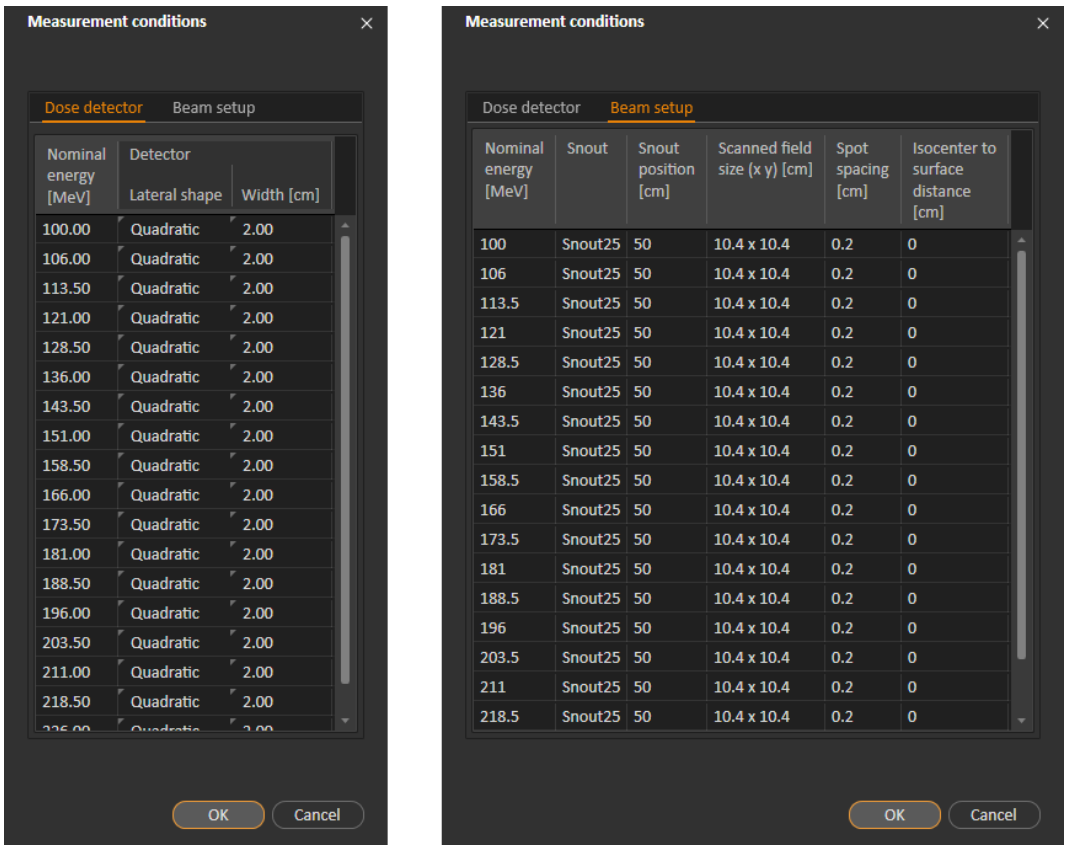

Measurement conditions
Dose detector
Beam setup
Nominal energy [MeV]
Detector
Lateral shape
Width [cm]
100.00 Quadratic 2.00
106.00 Quadratic 2.00
113.50 Quadratic 2.00
121.00 Quadratic 2.00
128.50 Quadratic 2.00
136.00 Quadratic 2.00
143.50 Quadratic 2.00
151.00 Quadratic 2.00
158.50 Quadratic 2.00
166.00 Quadratic 2.00
173.50 Quadratic 2.00
181.00 Quadratic 2.00
188.50 Quadratic 2.00
196.00 Quadratic 2.00
203.50 Quadratic 2.00
211.00 Quadratic 2.00
218.50 Quadratic 2.00
OK
Cancel
Measurement conditions
Dose detector
Beam setup
Nominal energy [MeV]
Snout
Snout position [cm]
Scanned field size (x y) [cm]
Spot spacing [cm]
Isocenter to surface distance [cm]
100 Snout25 50 10.4 x 10.4 0.2 0
106 Snout25 50 10.4 x 10.4 0.2 0
113.5 Snout25 50 10.4 x 10.4 0.2 0
121 Snout25 50 10.4 x 10.4 0.2 0
128.5 Snout25 50 10.4 x 10.4 0.2 0
136 Snout25 50 10.4 x 10.4 0.2 0
143.5 Snout25 50 10.4 x 10.4 0.2 0
151 Snout25 50 10.4 x 10.4 0.2 0
158.5 Snout25 50 10.4 x 10.4 0.2 0
166 Snout25 50 10.4 x 10.4 0.2 0
173.5 Snout25 50 10.4 x 10.4 0.2 0
181 Snout25 50 10.4 x 10.4 0.2 0
188.5 Snout25 50 10.4 x 10.4 0.2 0
196 Snout25 50 10.4 x 10.4 0.2 0
203.5 Snout25 50 10.4 x 10.4 0.2 0
211 Snout25 50 10.4 x 10.4 0.2 0
218.5 Snout25 50 10.4 x 10.4 0.2 0
OK
Cancel

Figure 156. In the **Measurement conditions** dialog it is possible to view beam setup information as well as to view and edit the detector information.

Results from dose computation

The results from the dose computation are displayed in a table as well as in two graphs showing the measured and computed absolute dose per meterset as well as the relative difference between measured and computed doses. The relative difference between the computed dose, d_{comp}, and the measured dose, d_{meas}, is defined as $(dose_{comp} - dose_{meas})/dose_{meas}$ and should not be more than 0.5%.

The displayed computed dose is extracted from a dose computation in a water phantom. The 3D dose in the water phantom is converted to a point dose, by interpolating the dose in the depth direction and averaging laterally over the detetctor width and center at the measurement point. The averaging is performed to decrease the effect of local fluctuations for the Monte Carlo dose computation. The uncertainty for the Monte Carlo absolute dosimetry calculation is obtained by first estimating the variance of the computed dose values for voxels within the detector width. From the

variance the standard error of the mean is calculated, which divided by the mean dose for the included voxels gives the displayed uncertainty.

Note: *There might be a slight difference in the results for the computed absolute doses for Monte Carlo, when computing all doses or just the dose for the selected energy. This is due to the fact that the random seed in the Monte Carlo dose computation will be different in the two cases. The difference will be of the same magnitude as the displayed statistical uncertainty.*

Note: *The relative difference will be 0.0% for the dose engine that was used for Auto modeling.*

Note: *If the relative difference for the PB dose engine is varying substantially over the energy range, it is an indication that MC was used for auto-modeling and that the number of histories was set too low.*

6.3 CHECKLIST BEFORE COMMISSIONING A PROTON PBS OR LINE SCANNING MACHINE

Before commissioning a proton PBS or Line scanning machine model, the following parameters shall be reviewed:

General

- Review all relevant information on the machine level with special care taken such that the beam line objects are correctly defined.
- Review the General and Scanning data tabs on the beam quality level (marked with 'PencilBeamScanning' or 'LineScanning').

General – measurement data

- Ensure that the measurements used as input to the model have a reasonable energy spacing. Energy spacing should not be more than 10 MeV for measured curves and absolute dosimetry.
- Check that MC and PB dose is calculated for all curves and absolute dosimetry (if both should be used).
- Go through all energies one by one and ensure that the calculated curves and absolute dosimetry match the measured curves and absolute dosimetry.

Spot Profiles

- Model parameters:
  - Check that the spot model divergence terms ($\overline{r\theta_0}$ =second parameter) are positive. Negative values give a strong indication that the direction of Z is misinterpreted.
  - Check that the spot size terms ($\sqrt{\overline{r^2}}$ = last parameter) are roughly in the order of 0.3 cm (highest energies) to 1.0 cm (lowest energies). Otherwise a wrong unit may have been used.
- Computed curves:
  - Resolution should be 0.1 cm.
  - Number of histories should be at least 1,000,000, but preferably 10,000,000.

Pristine Bragg peaks

- Beam data:
  - Check that the measured pristine Bragg peaks have been measured all the way to the surface (or at least 0.5 cm from surface).

  - Check that the size of the detector is 8.16 cm or 12 cm when single spot measurements are used.
  - Check that the size of the detector is not larger than 2 cm when scanned fields are used.

- Model parameters:
  - Go through all energy spectra one by one and make sure that the spectra are clean.
  - All intensities should be around the nominal energy.
  - If there are a lot of spikes towards lower energies, it is likely that a scanned field has been handled as a single spot measurement.
  - Check that the R80 Energy – Nominal Energy is not a large number (not much larger than a few MeV).

Computed curves

- Resolution should be 0.1 cm (0.15 cm could be OK if there is a memory problem):
  - Number of histories should be at least 400,000 for single spot measurements and at least 2000 for scanned fields.
  - Local relative errors should be less than ~1% with the exception of dose grid resolution problems at the lowest energies.

Absolute Dose

- Model parameters
  - Check that the Ions per MU is smooth. If there are kinks on the curve, it is likely that a measurement is bad or that a too high statistical uncertainty has been used in MC auto-modeling.

- Computed doses
  - Resolution should be at least 0.2 cm
  - Number of histories should be at least 50,000
  - Check that the statistical uncertainty in MC is less than ~0.2% for all energies
  - Check that the relative difference is less than ~0.5% for all energies (PB and MC)

    Note: *The relative difference will be 0.0% for the dose engine that was used for auto-modeling.*

    Note: *If the relative difference for the PB dose engine is very noisy, it is an indication that MC was used for auto-modeling and that the number of histories value was too low.*

Note: *Even if all parameters pass the review, the beam model needs to be properly validated. For more information, see warning 508815.*

7 NCT TREATMENT MACHINES

This chapter describes the machine properties for NCT treatment machines in the Beam Commissioning module. The parameters are shown in the right window when clicking the machine name in the machine tree view. The content of each tab is described in this section.

In this chapter

This chapter contains the following sections:

7.1	General properties	p. 310
7.2	NCT collimator	p. 312

Precaution

WARNING!

NCT machine commissioning. Commissioning of a machine in RayStation for a specific dose engine version should always be done in agreement with the treatment delivery system and dose engine manufacturer. (611928)

7.1 GENERAL PROPERTIES

This section describes the **General** tab in the Machine constraints workspace for NCT treatment machines.

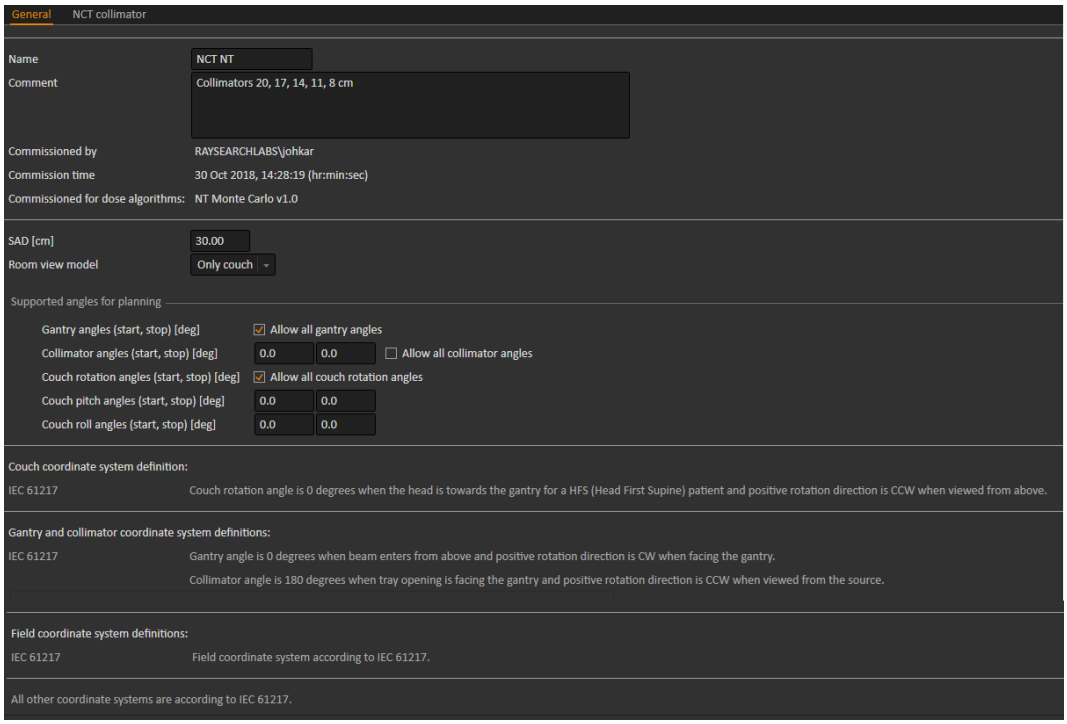

General
NCT collimator
Name
NCT NT
Comment
Collimators 20, 17, 14, 11, 8 cm
Commissioned by
RAYSEARCHLABS\johkar
Commission time
30 Oct 2018, 14:28:19 (hr:min:sec)
Commissioned for dose algorithms:
NT Monte Carlo v1.0
SAD [cm]
30.00
Room view model
Only couch
Supported angles for planning
Gantry angles (start, stop) [deg]
Allow all gantry angles
Collimator angles (start, stop) [deg]
0.0
0.0
Allow all collimator angles
Couch rotation angles (start, stop) [deg]
Allow all couch rotation angles
Couch pitch angles (start, stop) [deg]
0.0
0.0
Couch roll angles (start, stop) [deg]
0.0
0.0
Couch coordinate system definition:
IEC 61217
Couch rotation angle is 0 degrees when the head is towards the gantry for a HFS (Head First Supine) patient and positive rotation direction is CCW when viewed from above.
Gantry and collimator coordinate system definitions:
IEC 61217
Gantry angle is 0 degrees when beam enters from above and positive rotation direction is CW when facing the gantry.
Collimator angle is 180 degrees when tray opening is facing the gantry and positive rotation direction is CCW when viewed from the source.
Field coordinate system definitions:
IEC 61217
Field coordinate system according to IEC 61217.
All other coordinate systems are according to IEC 61217.

Figure 157. The **General** tab.

Name

This is the name of the treatment machine which will be shown in the GUI and exported to DICOM. The name cannot be longer than 16 characters. The name of uncommissioned, template and commissioned machines must be unique.

Saved by / Saved time

These properties will be shown for uncommissioned machines the last time the machine was saved.

SAD [cm]

The source axis distance (SAD) in cm. For the definition of SAD for an NCT treatment machine, see Figure 159.

Room view model

This selection decides how the machine is visualized in the Room View. For NCT treatment machines the room view will always only display the couch ("Only couch").

Supported gantry angles (start, stop) [deg]

This property sets the allowed angles for radiation treatment. Typically, an NCT machine has a fixed beam line. In that case, the machine only has one supported gantry angle.

Supported collimator angles (start, stop) [deg]

This property sets the allowed collimator angles for radiation treatment. As NCT treatment machines have a circular collimator, the value of this property has no impact.

Supported couch rotation angles (start, stop) [deg]

This property sets the allowed couch rotation angles for radiation treatment.

Couch pitch angles (start, stop) [deg]

This property sets the allowed couch pitch angles for radiation treatment.

Couch roll angles (start, stop) [deg]

This property sets the allowed couch roll angles for radiation treatment.

The couch coordinate system

For NCT treatment machines the only supported couch coordinate system is IEC 61217. The couch rotation angle is zero when the head is towards the gantry in the head first orientations. The couch angle increases counter-clockwise when looking from above.

The pitch angle of the couch is zero when the patient is lying flat on the couch. Positive rotation direction is such that the head of an HFS (Head First Supine) patient is raised higher than the feet.

The roll angle of the couch is zero when the patient is lying flat on the couch. Positive rotation direction is such that the right side of an HFS (Head First Supine) patient is raised higher than the left side.

The gantry and collimator coordinate system

For NCT treatment machines the only supported gantry coordinate system is IEC 61217. The IEC 61217 gantry coordinate system has gantry angle zero when the beam enters from above and positive rotation direction clockwise when facing the gantry. The collimator is not allowed to rotate for NCT treatment machines and is always set to 0.

The field coordinate system

For NCT treatment machines the only supported field coordinate system is IEC 61217.

7.2 NCT COLLIMATOR

This section describes the **NCT collimator** tab in the Machine constraints workspace for NCT treatment machines.

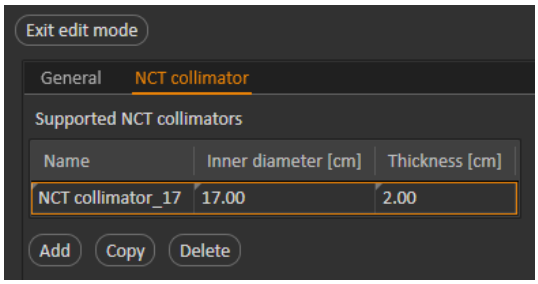


Figure 158. The **NCT collimator** tab.

Add, copy and delete

Use the **Add**, **Copy** and **Delete** buttons to add the supported NCT collimators to the list.

Collimator dimensions

The definition of the inner diameter and thickness of the collimator is illustrated in Figure 159.

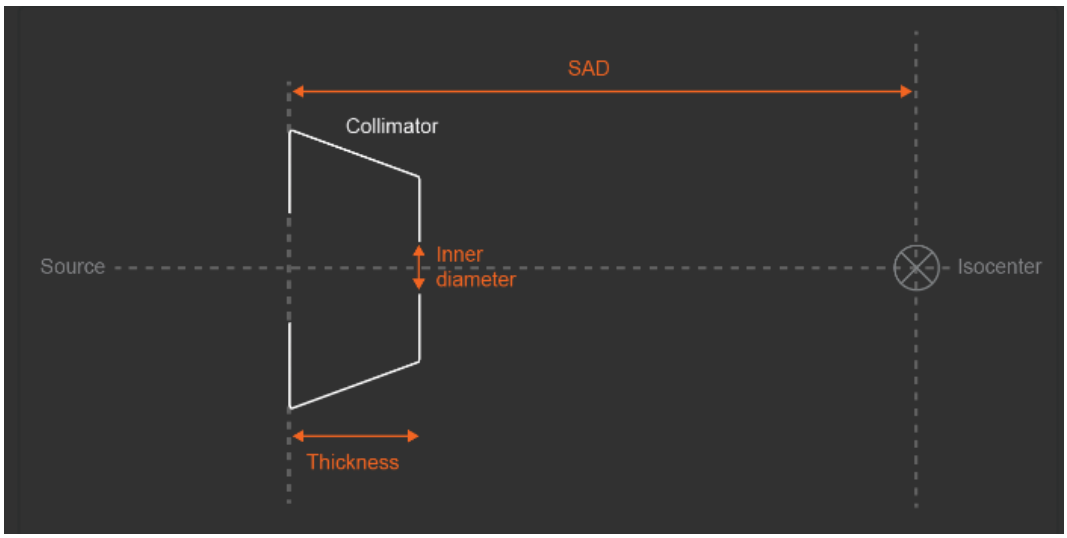


Figure 159. The definition of the collimator dimensions and SAD for an NCT treatment machine.

8 THE BEAM 3D MODELING MODULE

The Beam 3D Modeling module provides tools for importing, modifying and approving phantom data for use in the RayStation QA Preparation module. The module also contains tools for performing photon and electron dose computations using uncommissioned machines. It is possible to create and calculate dose on 3D-CRT plans for photons as well as on electron plans. It is also possible to calculate dose on imported plans, including photon plans with arbitrary treatment techniques. The graphical user interface in the Beam 3D Modeling module is similar to the 3D-CRT Beam Design and Electron Beam Design modules in the RayStation application for photons and electrons respectively. See the *RSL-D-RS-9A-USM, RayStation 9A User Manual* for more information.

Beam 3D Modeling does not support test plans for other modalities than photons and electrons.

In this chapter

This chapter contains the following sections:

8.1	The Beam 3D Modeling module user interface	p. 314
8.2	Phantom handling	p. 315
8.3	Plan setup	p. 325
8.4	Photon beam design	p. 332
8.5	Electron beam design	p. 342
8.6	Working with uncommissioned machines	p. 349

8.1 THE BEAM 3D MODELING MODULE USER INTERFACE

The Beam 3D Modeling workspace contains several views showing the Beam's Eye View (BEV), 2D and 3D views, DVHs and Line dose view.

The workspace also contains three sub-windows showing 2D image data in a specific patient plane, making it possible to simultaneously work in three dimensions. One of the two sub-windows to the right shows Dose Statistics and Plan info.

The lower part of the workspace displays the beam list, which contains the tabs Beams, Control points, Beam weighting and Beam specification points. At the borders between the different views are handles which can be dragged to adjust the workspace as desired.

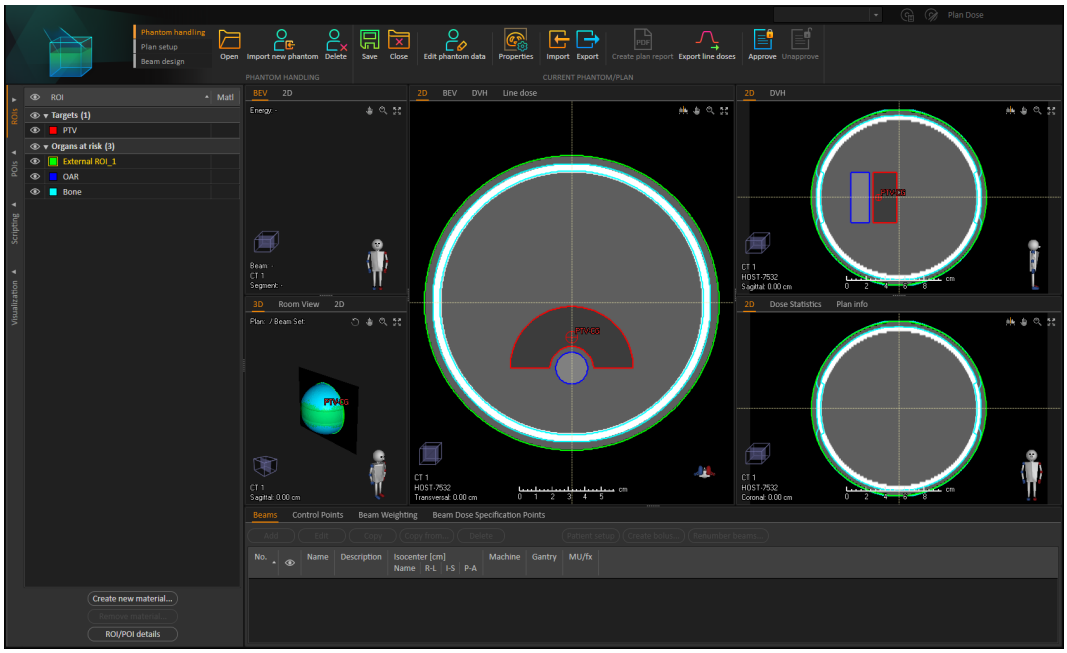


Figure 160. The Beam 3D Modeling workspace.

8.2 PHANTOM HANDLING

The **Phantom handling** tab contains tools for opening, editing, importing, exporting and saving of patient (phantom) data. These tools are described in detail in the Patient Data Management chapter in the *RSL-D-RS-9A-USM, RayStation 9A User Manual*.

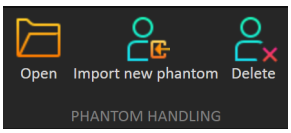


Figure 161. The Phantom handling toolbar.

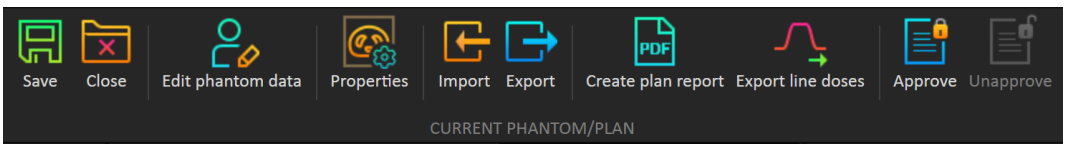
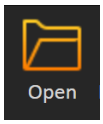


Figure 162. The Current phantom/plan toolbar.

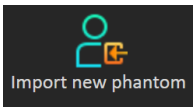
8.2.1 Open phantom data

To open phantom data, click the **Open** button.



8.2.2 Importing phantom data

To import a phantom to the RayPhysics 9A database, click the **Import new phantom** button.



This opens the DICOM import dialog. For more information about DICOM import, see the *RSL-D-RS-9A-USM, RayStation 9A User Manual*.

RayPhysics 9A can import the following DICOM data:

- DICOM Images (CT)
- Structure set (RT Struct)
- Plan (RT Plan)
- Dose (RT Dose)

Note: *Patients/phantoms imported to RayPhysics 9A will not be visible in the RayStation application and vice versa.*

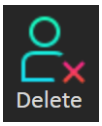
Note: *Approval status in the DICOM data is kept in the Beam 3D Modeling module. If a phantom with an approved structure set is imported, it will not be possible to edit ROIs or POIs. If a phantom with an approved plan is imported, it will not be possible to edit ROIs or POIs or change the CT-to-density table, and therefore it will not be possible to calculate dose and approve the phantom for use in the RayStation QA Preparation module.*

8.2.3 Exporting phantom data

It is possible to DICOM export CT, structure sets, created 3D-CRT and electron plans and calculated dose. The DICOM attribute Plan intent will be set to 'RESEARCH' when exporting from the Beam 3D Modeling module.

8.2.4 Delete phantom data

To delete a phantom or a plan from the RayPhysics 9A database, click the **Delete** button.

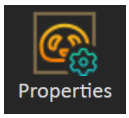


Only phantoms that are not approved can be deleted.

Note: *Deleting a phantom that has been used for a verification plan in RayStation will disable DICOM export of the verification plan from the QA Preparation module in RayStation with QA plan patient identity set to Phantom.*

8.2.5 Changing image set properties

Click the **Properties** button to open the Image Set Properties dialog.



For CT Image sets, it is possible to edit the **Image set name** and the Imaging system. The imaging system is connected to an image set type, for example CT. The imaging system specifies which CT to density table that will be used to determine the densities in the image data.

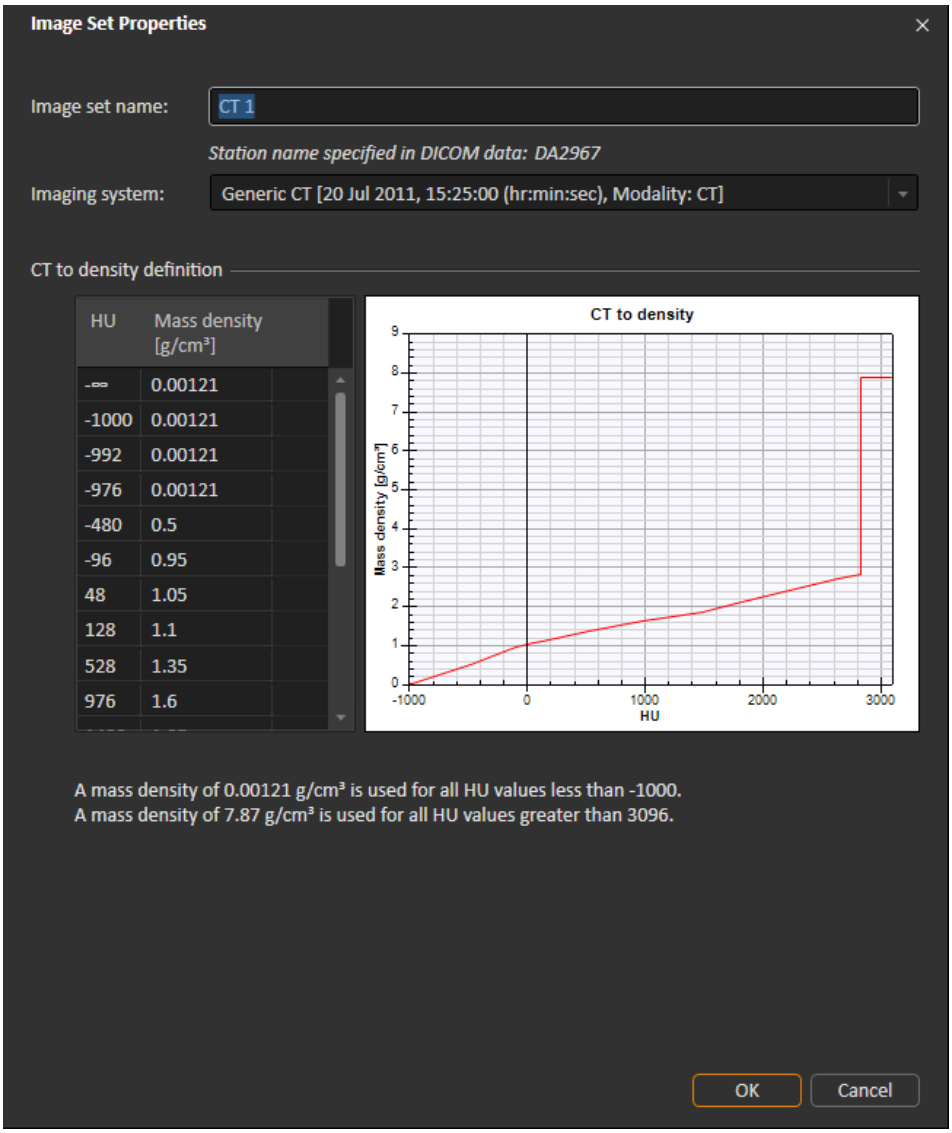


Figure 163. The Image Set Properties dialog where the Image set name and the CT to density table are displayed.

8.2.6 Export line doses

Any added line doses can be exported to a csv file.

To export line doses:

1. Click the **Export line doses** button in the toolbar.

2. In the Save As dialog that opens, select a directory, type a name for the file, and click Save.

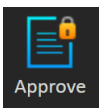
For more information about the file format, refer to the *RSL-D-RS-9A-USM, RayStation 9A User Manual*.

8.2.7 Approve phantom

To use a phantom for creating verification plans in the RayStation QA Preparation module it must be approved. Before a phantom can be approved it must fulfill some requirements. These are:

- An External ROI must have been specified for the image set.
- A CT to density table must have been specified for the image set.
- It is recommended (but not required) to define a localization point.
- The patient position must be HFS.

To approve the phantom, click the **Approve** button.



To unapprove the phantom, click the **Unapprove** button.

Note: *In RayStation 9A, it is possible to unapprove phantoms used for verification plans in the RayStation QA Preparation module. To be able to DICOM export the verification plan from the QA Preparation module with QA plan patient identity set to Phantom, the phantom may not be deleted from RayPhysics.*

Note: *Once approved, a phantom is read only and it will not be possible to edit the phantom at the time of verification plan creation in the RayStation QA Preparation module. Therefore, it is not possible to move the phantom with respect to the couch when creating verification plans in RayStation, which may be especially important for TomoHelical and TomoDirect plans. It is possible to approve multiple instances of a phantom with different positions in relation to the couch.*

8.2.8 ROIs and POIs

It is not possible to add ROIs or POIs or edit ROI contours in the Beam 3D Modeling module but it is possible to edit ROI or POI type and name and ROI material.

Note: *In order to use a CT with a couch replacement when importing a plan from Precision, the couch ROI must be added in RayStation as a support-type ROI. Import the CT images and structure set to the Beam 3D Modeling module and then import the plan from iDMS.*

8.3 PLAN SETUP

The **Plan setup** tab contains buttons for creating, editing and copying a plan as well as buttons for modifying the dose grid. Only unapproved phantoms can be used.

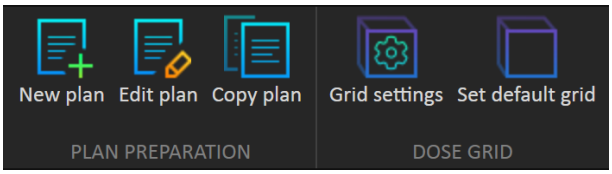
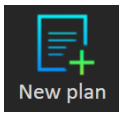


Figure 164. The Plan setup toolbar.

8.3.1 Create new plan

To create a new plan, click the **New plan** button.



This opens the New plan dialog.

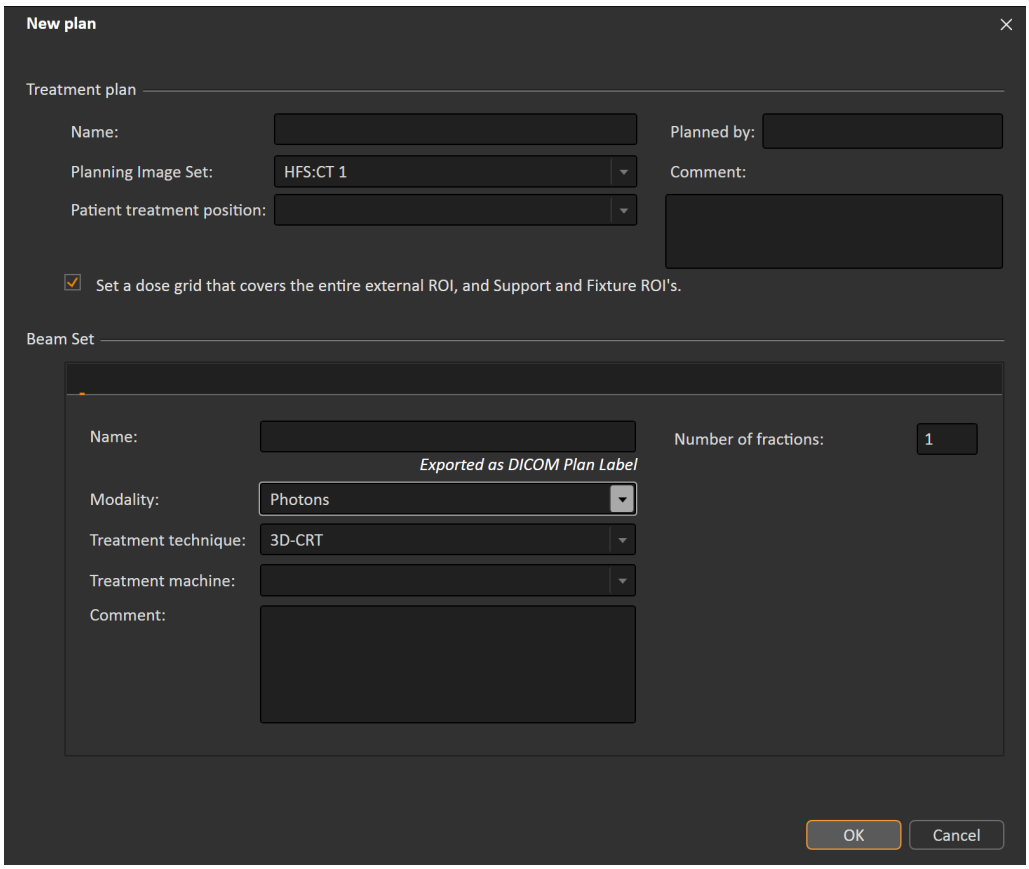


Figure 165. The New plan dialog.

1. Enter a Name for the plan.

   Note: *The plan name is exported as DICOM RT Plan Name [300A,0003].*

2. Select **Planning image set** from the drop-down list to use as a basis for the treatment plan.
3. Select **Patient treatment position**.
4. Enter a **Comment** in free text (optional).

5. Select to **Set a dose grid that covers the entire external ROI, and Support and Fixture ROIs** by checking the corresponding check box (this is checked by default if an External ROI has been assigned to the patient).

   Note: *The radiation set name is exported as DICOM RT Plan Label [300A, 0002].*

6. Enter **Number of fractions**. Default is 1 in the Beam 3D Modeling module.
7. Select **Modality**. Photons and electrons are available.
8. Select **Treatment technique**. The only option is 3D-CRT for photons and Cutout and Applicator for electrons.
9. Select **Treatment machine**. The list contains both commissioned and uncommissioned treatment machines. Uncommissioned machines are listed with "[Uncommissioned]" after the name instead of commissioning time.
10. Enter a **Comment** in free text (optional).
11. Click **OK**. The plan (without beams) is opened. The image set selected for the plan is displayed in the patient views.

Add beams

Beams can be added from the beam list at the bottom of the workspace. Click the **Add** button to open the **Add Beam** dialog. See the Plan Design chapter in the *RSL-D-RS-9A-USM, RayStation 9A User Manual* for more information.

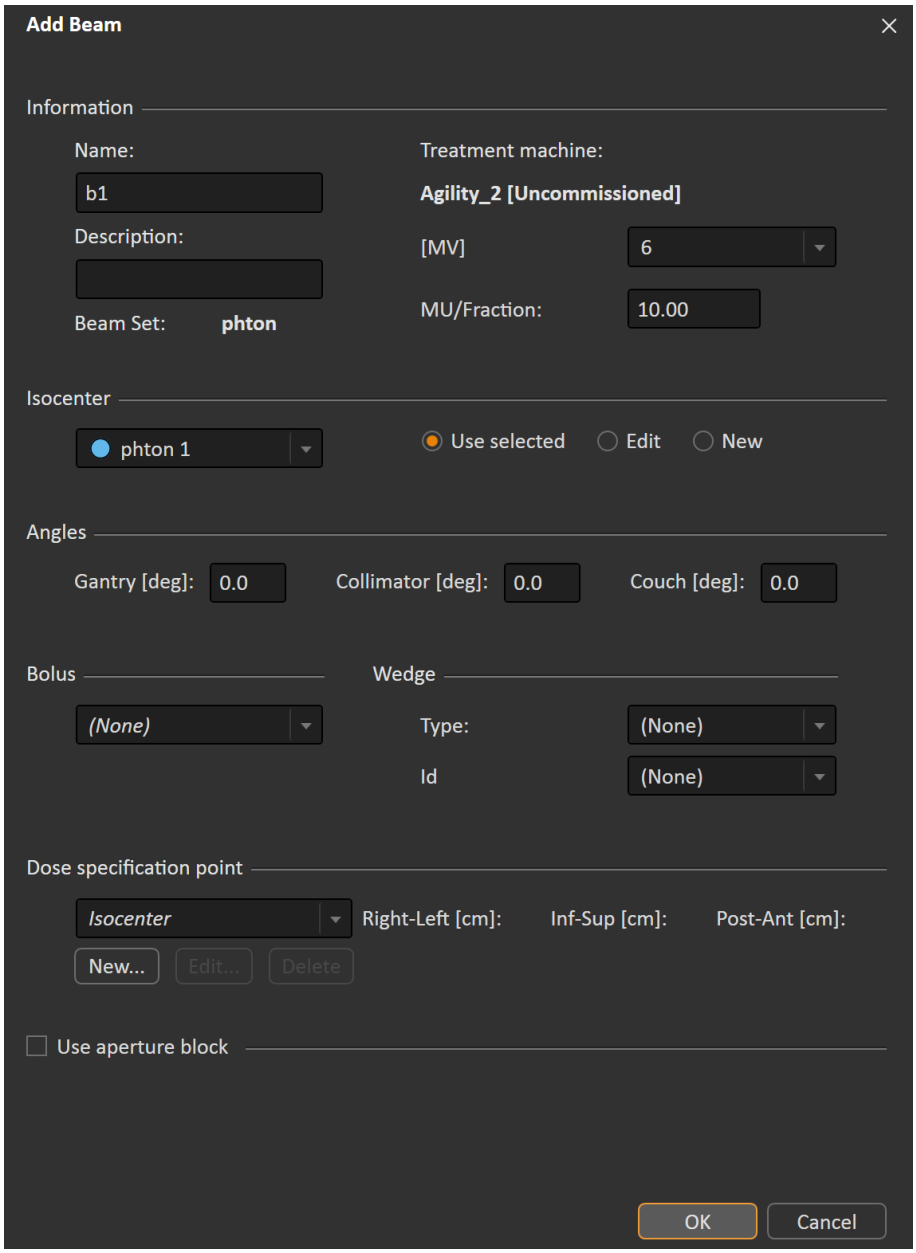
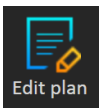


Figure 166. The **Add Beam** dialog.

A prescription cannot be defined in the Beam 3D Modeling module, instead the user can define MU/fraction for each beam in the **Add Beam** dialog.

Edit plan settings

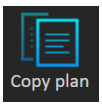
To edit plan settings click the **Edit plan** button. This opens the Edit Plan dialog.



If the plan is an imported non-3D-CRT plan, the Treatment technique drop-down list will be empty. To keep the control points of the imported plan, do not change this setting.

Copy plan

To make a copy of the current plan, click the **Copy plan** button.

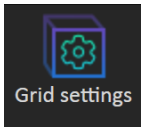


In the Copy Plan dialog, enter a name for the new plan and click **OK**. The new plan will be opened as the selected current plan, i.e. the plan that is displayed in the workspace.

8.3.2 Defining the dose grid

The dose grid is the 3D grid in which the dose distribution is calculated. To edit the dose grid:

1. Click the **Grid settings** button.



This opens the Edit Dose Grid dialog.

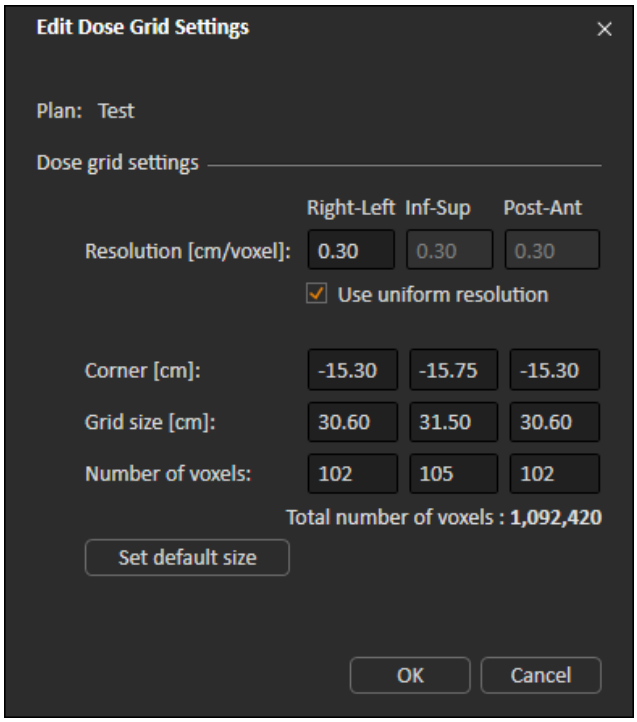


Figure 167. The Edit Dose Grid Settings dialog.

2. Enter **Resolution** values. This is the size of the voxels in the dose grid. Uncheck the **Use uniform resolution** check box to define individual values per direction. The default resolution is specified in ClinicSettings, see Appendix D in the *RSL-D-RS-9A-USM, RayStation 9A User Manual*.
3. Select to enter **Corner** value, **Grid size** and/or **Number of voxels**.
4. Click the **Set default size** button to create a grid that covers the entire External geometry, support and fixture ROIs.
5. Click **OK**.

Set default grid

Clicking the **Set default grid** button in the toolbar sets a grid, of the current resolution, that covers the entire External geometry, patient support, fixation and bolus referenced from the plan.

Note: *The exact size of the grid is dependent on the resolution, since the grid is always divided into whole pixels.*

8.4 PHOTON BEAM DESIGN

The **Beam design** tab contains buttons for creating rectangular fields, computing dose and creating blocks.

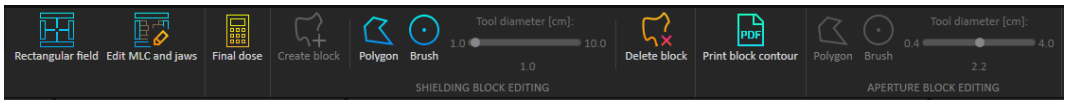


Figure 168. The Beam design toolbar for photon beams.

8.4.1 Create rectangular field

To create a rectangular field:

1. Click the **Create rectangular field** button.

This opens the Create rectangular field dialog.

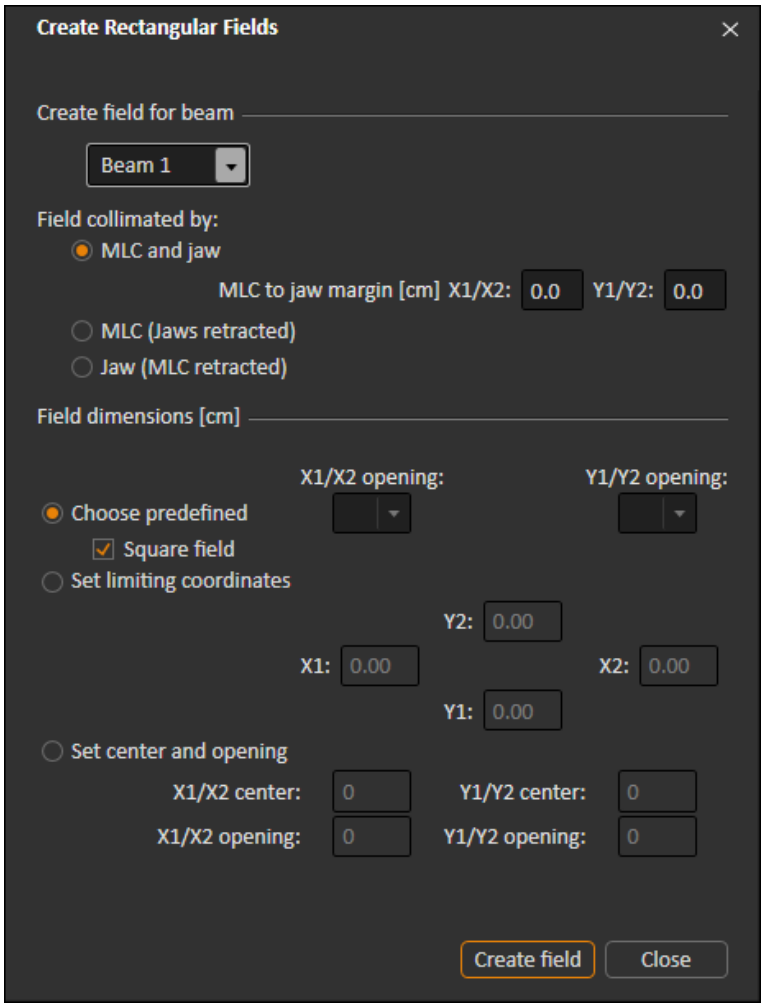
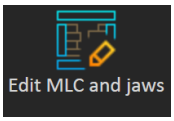


Figure 169. The Create rectangular field dialog.

2. Select the beam to create the field for in the **Create field for beam** list.
3. Select if the field should be collimated by; **MLC and jaw, MLC (Jaws retracted)** or **Jaw (MLC retracted)**.
4. Set **Field dimensions**. The options are: Choose predefined, Set limiting coordinates and Set center and opening.
5. Click **Create field**.

8.4.2 Edit segment shapes

Click the **Edit MLC and jaws** button.



This opens the Edit MLC and jaws dialog which provides several tools to manually edit the segment shape.

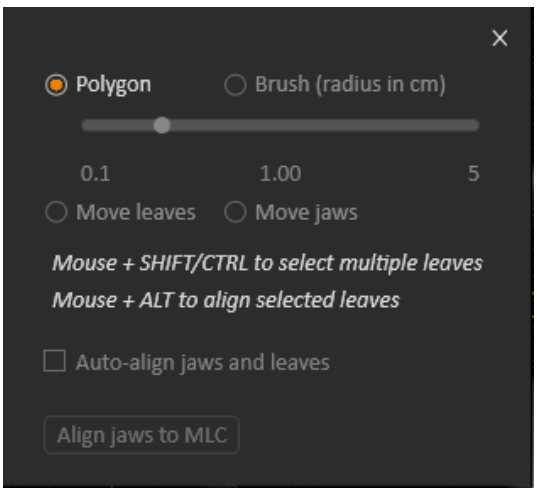


Figure 170. The Edit MLC and jaws dialog.

- Use the **Polygon** tool to manually draw a polygon shape in the BEV. Right-click in the view to close the polygon shape.
- Use the **Brush** tool to push the leaves in the BEV to a desired position. The size of the ball can be adjusted using the slider in the Editing window, by pressing the + and - keys on the numerical keyboard, or by using the mouse wheel while pressing the ALT key. (By using the smallest size of the ball individual leaves can be moved.)
- Use the **Move leaves** tool to manually pull the leaves to a desired position. Left-click and press SHIFT/CTRL to select multiple leaves. Left-click and press ALT to align the selected leaves.
- Use the **Move jaws** tool to manually pull the jaws in the BEV to desired positions. Click with the mouse on the (blue) jaw to move it.
- Uncheck **Auto-align jaws and leaves** to move leaves without affecting jaws with the **Brush** tool, or jaws without affecting leaves with the **Move jaw** tool.
- Click the **Align jaws to MLC** button to align the jaws with the MLC opening.

Note: *Although it is possible to manually move a jaw and thereby collimate using the jaws also inside a field, this is not advisable. E.g., for an Elekta machine where the x-jaw is relatively thin compared with an MLC leaf, the jaw collimation will not be very effective.*

8.4.3 Calculate dose

Dose computation can be performed using the buttons in the **Dose computation** toolbar located under the **Computation** tab in the Beam 3D Modeling workspace.

Click the **Final dose** button to calculate the final dose.

Note: *All doses computed in RayPhysics 9A will be non-clinical since doses may be calculated with an uncommissioned machine.*

8.4.4 Shielding blocks

Block shapes can be generated based on ROI projections and can be manually edited in the BEV.

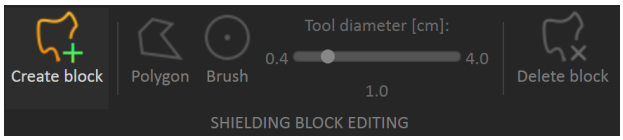
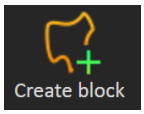


Figure 171. The Block editing tools.

Create blocks

To create a block:

1. Click the **Create block** button.

   This opens the **Create Block** dialog.

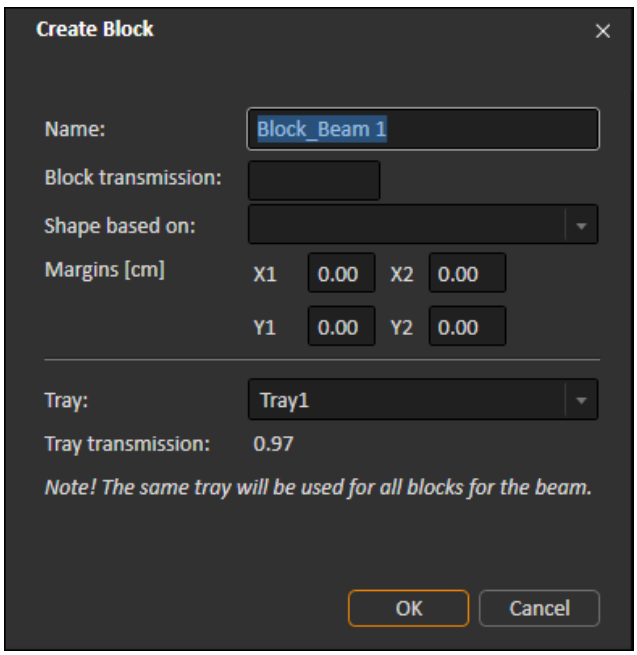
   

   Figure 172. The **Create Block** dialog.

2. Enter a **Name** for the block.
3. Enter **Block transmission**.

4. Select an ROI from the drop-down list that the block shape will be based on.
5. Set block **Margins**.
6. Select **Tray**.
7. Click **OK**. The block is created and the block properties (Name, Block transmission and tray) are displayed in the Beams list.

Edit the block contour

The block shape can be edited in the BEV using the **Polygon** or **Brush** tool.

- **Brush**: The size of the ball can be adjusted using the slider in the **Block editing** toolbar, by pressing the + and - keys on the numerical keyboard, or by using the mouse wheel while pressing the ALT key. The smallest diameter of the brush is set to the milling tool diameter for the block.
- **Polygon**: Crossing contours are not allowed. A new contour is added to the original contour if the starting point is inside a contour on its edge, and finish point is inside the same contour. A new contour is subtracted from the original contour if the starting point is outside a contour on its edge, and the finish point is outside the same contour. If defining a two point polygon with both points outside the current aperture shape, and the line intersecting it twice, the smaller half will be cut off.

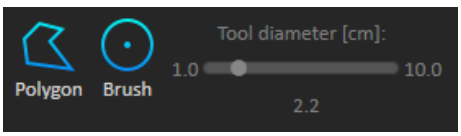
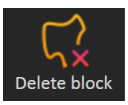


Figure 173. The Block editing tools.

Delete blocks

To delete a block, click the **Delete block** button.



Print block contour

A block contour can be printed in its actual size on an office printer. Click the **Print block contour** button.

8.4.5 Aperture blocks

Aperture blocks have to be defined for each beam when creating or editing a beam.

To enable aperture blocks:

1. Select a beam in the beam list.
2. Double-click the beam or click the **Edit** button. This opens the **Edit Beam** dialog.

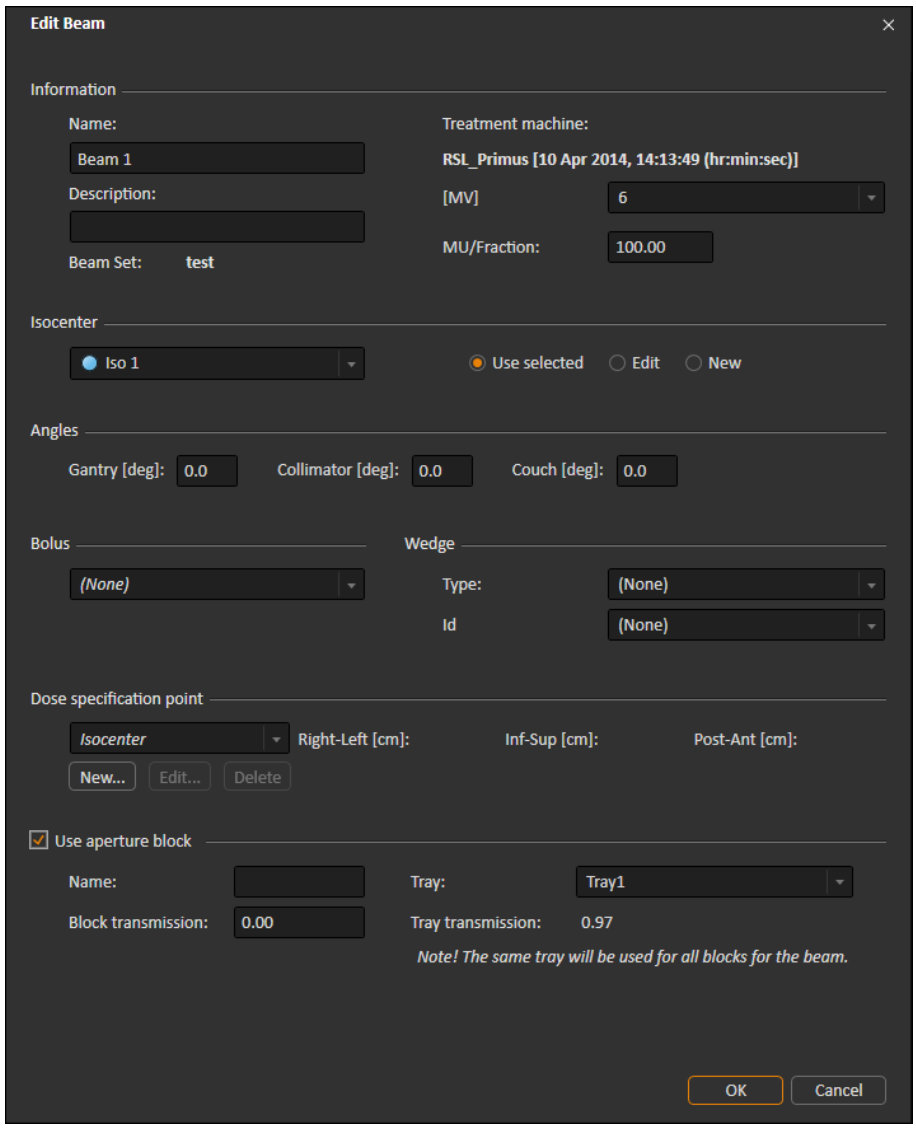


Figure 174. The **Edit Beam** dialog.

3. Check the **Use aperture block** check box.
4. Enter a block **Name**.
5. Select **Tray**.
6. Enter **Block transmission**.
7. Click **OK**.

Edit the block contour

The block shape can be edited in the BEV using the **Polygon** or**Brush** tool.

- **Brush**: The size of the ball can be adjusted using the slider in the **Block editing** toolbar, by pressing the + and - keys on the numerical keyboard, or by using the mouse wheel while pressing the ALT key. The smallest diameter of the brush is set to the milling tool diameter for the block.
- **Polygon**: Crossing contours are not allowed. A new contour is added to the original contour if the starting point is inside a contour on its edge, and finish point is inside the same contour. A new contour is subtracted from the original contour if the starting point is outside a contour on its edge, and the finish point is outside the same contour. If defining a two point polygon with both points outside the current aperture shape, and the line intersecting it twice, the smaller half will be cut off.

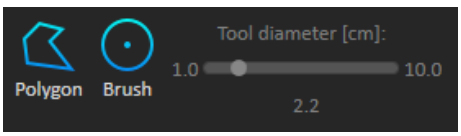


Figure 175. The Block editing tools.

Remove aperture block contour

To remove the aperture block from the beam, uncheck the **Use aperture block** check box.

Print cutout contour

A block contour can be printed in its actual size on an office printer. Click the **Print cutout contour** button.

8.5 ELECTRON BEAM DESIGN

The **Beam design** tab contains buttons for designing cutout contours and computing dose.

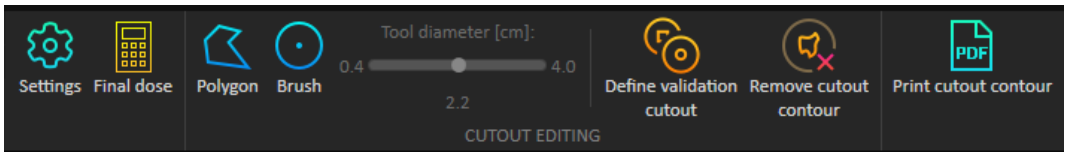
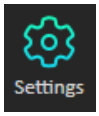


Figure 176. The Beam design toolbar for electron beams.

8.5.1 Dose computation settings

To edit the dose computation settings:

1. Click the **Settings** button.



2. This opens the Dose Computation Settings dialog.

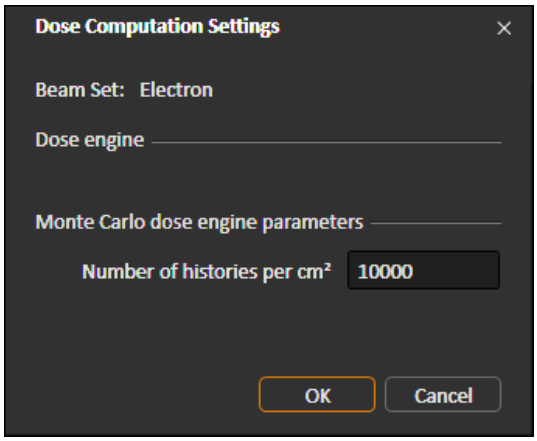


Figure 177. The Dose Computation Settings dialog.

3. Enter **Number of histories per cm²** to be used per beam for the electron beams in the beam set. The lower limit is 1000 per cm^2.
4. Click **OK**.

Note: *Changing the number of histories does not invalidate calculated dose. If the number of histories is changed after a clinical dose has already been computed, it will not be possible to re-calculate dose based on the updated number of histories without first invalidating the dose manually. If a non-clinical dose exists, changing the number of histories and re-calculating dose will result in a new dose being calculated based on the changed number of histories.*

8.5.2 Calculate final dose

A final dose can be calculated using the electron Monte Carlo dose engine. Click the **Final dose** button or type Ctrl + D to calculate the clinical dose.

The electron Monte Carlo dose engine is described in detail in the *RSL-D-RS-9A-REF, RayStation 9A Reference Manual*.

Note: *All doses computed in RayPhysics 9A will be non-clinical since doses may be calculated with an uncommissioned machine.*

8.5.3 Cutout editing

Cutouts have to have been defined for each beam when creating the beam. See the Plan Design chapter in the *RSL-D-RS-9A-USM, RayStation 9A User Manual* for more information.

Edit the cutout contour

The cutout contour can be edited in the BEV using the **Brush** tool or the **Polygon** tool.

- **Polygon**: A new contour is added to the original contour if the starting point is inside a contour on its edge, and finish point is inside the same contour. A new contour is subtracted from the original contour if the starting point is outside a contour on its edge, and the finish point is outside the same contour. If defining a two point polygon with both points outside the current aperture shape, and the line intersecting it twice, the smaller half will be cut off. Crossing contours are not allowed.
- **Brush**: The size of the ball can be adjusted using the slider in the **Block editing** toolbar, by pressing the + and - keys on the numerical keyboard, or by using the mouse wheel while pressing the ALT key. The smallest diameter of the brush is set to the milling tool diameter for the block.

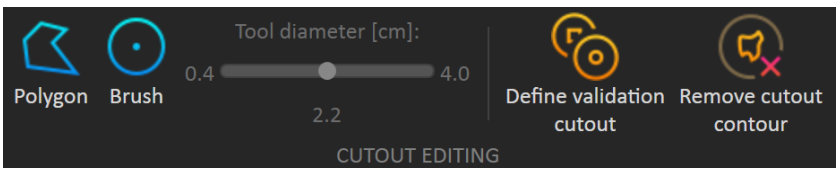
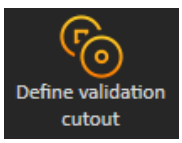


Figure 178. The cutout editing tools.

Define validation cutout

To define a validation cutout:

1. Click the **Define validation cutout** button.

   This opens the Define validation cutout dialog.

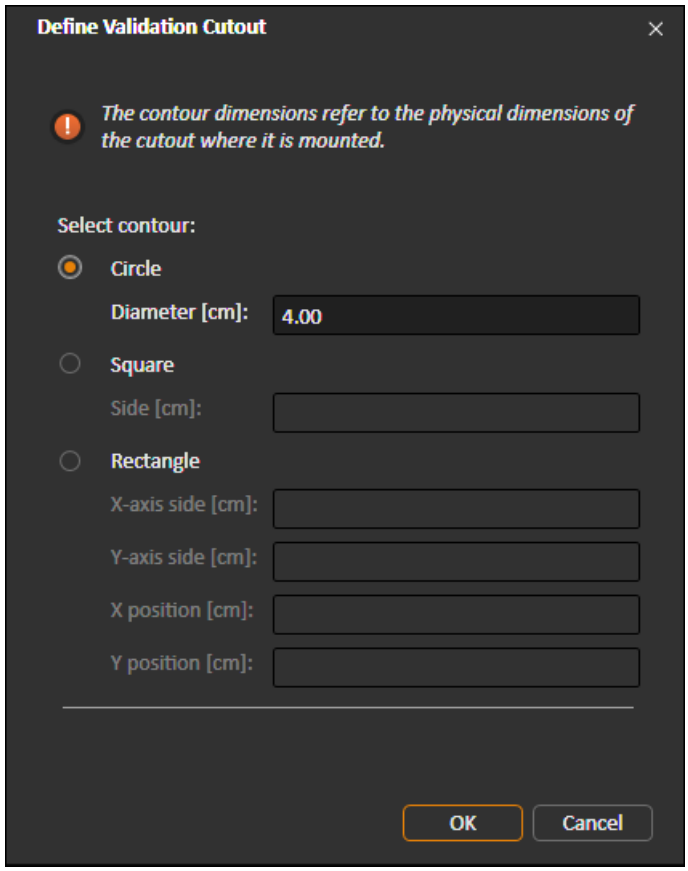


Figure 179. The Define validation cutout dialog.

2. Select contour. Available block contour shapes are:
   - **Circle** – centered around the isocenter.
   - **Square** – centered around the isocenter.
   - **Rectangle** – the X and Y positions refer to the lower left corner of the rectangle, where the X and Y axes are aligned with those of the Beam limiting device coordinate system.

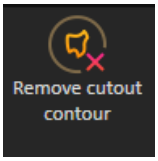
   Note: *The contour dimensions here are defined in the physical downstream plane of the cutout, i.e. not in the isocenter plane.*

   Note: *The rectangle is defined in the IEC 61217 beam limiting device coordinate system and is not affected by the jaw labeling standard selected in RayPhysics.*

3. Click **OK**.

Remove cutout contour

To clear the cutout contour, click the **Remove cutout contour** button.



8.5.4 Print cutout contour

A cutout contour can be printed in its actual size on an office printer. This is done by first creating a cutout report in PDF format and then printing the PDF file using an office printer.

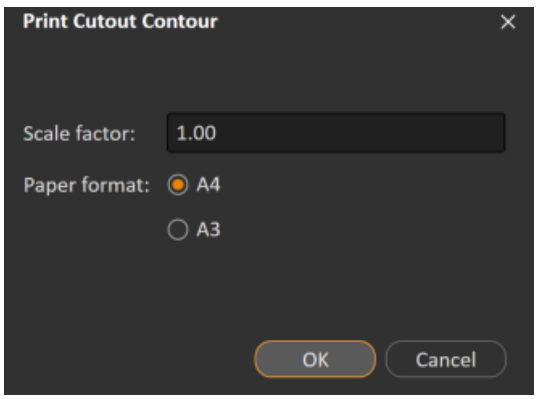
WARNING!

Verify the scale of the block/cutout printout. The printer settings will affect the actual size of the block/cutout in the printout. Before using the block/cutout printout for block/cutout manufacturing or verification, always check that the scale of the x- and y-axes are equal and that 1 cm on the verification scale corresponds to 1 cm using a ruler. (508818)

To print a cutout contour:

1. Click the **Print cutout contour** button.

This opens the **Print Cutout Contour** dialog.



2. Set a **Scale factor** (default value is 1).
3. Select **Paper format** (A4 or A3).
4. Click **OK**. A cutout report will be created in the PDF format.

8.6 WORKING WITH UNCOMMISSIONED MACHINES

It is possible to use an uncommissioned machine for plan generation in the Beam 3D Modeling module which means that a machine selected for a plan may be changed after the plan was created. It is mandatory to save changes before switching from the Beam Commissioning or CT Commissioning modules to the Beam 3D Modeling module or vice versa. It is however possible to have a machine in edit mode when switching to the Beam 3D Modeling module.

Uncommissioned machines will be listed with [Uncommissioned] instead of commissioning time in the Treatment machine list.

8.6.1 The machine has been updated after the plan was created

If a beam model parameter not affecting the plan but affecting the dose is changed, the user will get the message that the dose must be invalidated in order to update the machine reference to the latest version of the machine.

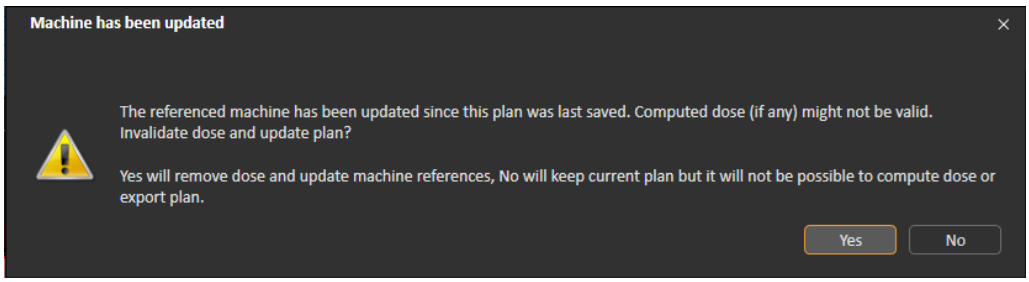

Machine has been updated
The referenced machine has been updated since this plan was last saved. Computed dose (if any) might not be valid. Invalidate dose and update plan?
Yes will remove dose and update machine references, No will keep current plan but it will not be possible to compute dose or export plan.
Yes
No

Figure 180. Warning dialog. The machine has been updated after the plan was saved.

Selecting **Yes** will invalidate the dose and update the machine reference. Selecting **No** means keeping the dose visible, but it is not possible to calculate new dose or DICOM export the plan and dose without updating the machine reference to the latest version. If selecting **No** and opening the Edit plan dialog, no machine will be selected in the **Treatment machine** drop down list. To switch to the latest version of the machine, locate the uncommisioned machine with the same name in the list.

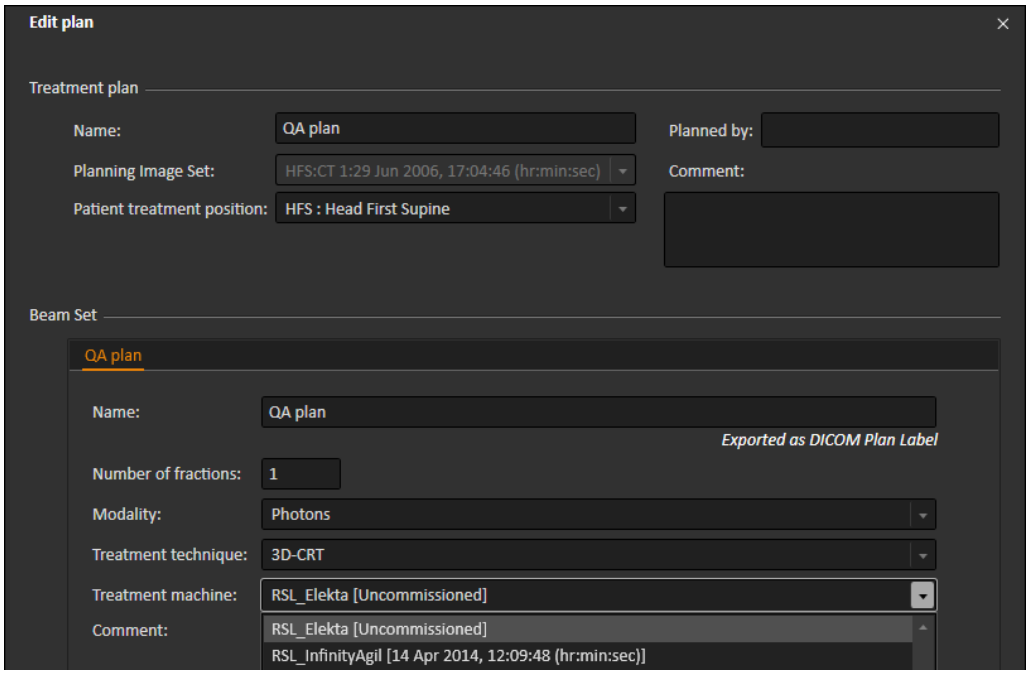


Figure 181. Both commissioned and uncommissioned machines are available in the Treatment machine drop-down list. Uncommissioned machines will be listed with [Uncommissioned] after the name instead of commissioning time.

8.6.2 The plan is not compatible with the machine

If a selected uncommissioned machine is changed so that it is no longer compatible with the plan, both dose and control points will be invalidated.

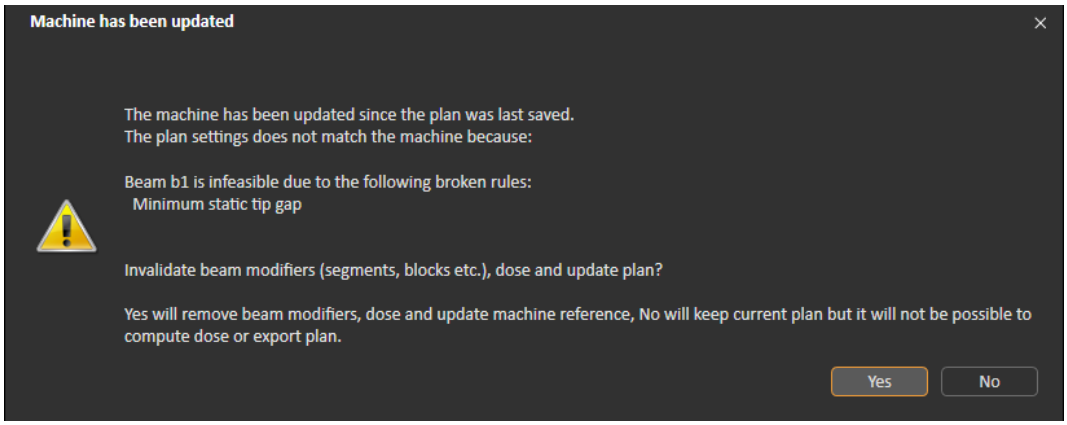

Machine has been updated
The machine has been updated since the plan was last saved.
The plan settings does not match the machine because:
Beam b1 is infeasible due to the following broken rules:
Minimum static tip gap
Invalidate beam modifiers (segments, blocks etc.), dose and update plan?
Yes will remove beam modifiers, dose and update machine reference, No will keep current plan but it will not be possible to compute dose or export plan.
Yes
No

Figure 182. Warning dialog. The plan is not compatible with the machine.

Selecting **Yes** will clear the control points and update the machine reference. Selecting **No** will keep the control point and dose but it will not be possible to calculate new dose or to DICOM export the plan and dose without updating the machine reference to the latest version.

For certain changes to electron beam qualities, the plan will be updated automatically. If any beam is infeasible after the change, all beams will be removed.

9 THE CT COMMISSIONING MODULE

The CT Commissioning module is used to enter CT and CBCT information, both of which will be referred to as CTs in this chapter.

In this chapter

This chapter contains the following sections:

9.1	The CT tree view	p. 354
9.2	Operations on CTs	p. 357
9.3	The CT Commissioning module workspace	p. 358
9.4	Enable laser export	p. 364

Precaution

WARNING!

CT to density calibration for proton and carbon ion plans. In RayStation, the same CT to mass density calibration curve is used for proton and carbon ion dose calculations as for photon dose calculations. Note that the requirement on a correct CT calibration is considerably higher for proton and carbon ion dose calculations than for photon dose calculations. CT calibration validated for photon or electron use may not be sufficient for ion dose calculation. (371600)

9.1 THE CT TREE VIEW

The CT tree view shows the available machines. Select to view a CT by clicking at the machine name.

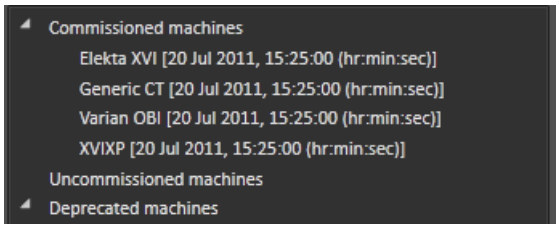

Commissioned machines
Elekta XVI [20 Jul 2011, 15:25:00 (hr:min:sec)]
Generic CT [20 Jul 2011, 15:25:00 (hr:min:sec)]
Varian OBI [20 Jul 2011, 15:25:00 (hr:min:sec)]
XVIXP [20 Jul 2011, 15:25:00 (hr:min:sec)]
Uncommissioned machines
Deprecated machines

Figure 183. The CT tree view.

When opening the CT Commissioning module the CT tree view shows the available CTs in the machine database. From this state the CTs are changed locally by the user.

9.1.1 Save to and read from database

CTs are saved to the machine database at save, commissioning, deprecate or delete and optionally at exit edit mode. Saving CT requires synchronization with the machine database, which may have been changed by another user. The synchronization can also be forced by clicking the **Refresh machine list** button at the bottom of the machine list workspace.

Opening a CT in edit mode also triggers an automatic synchronization with the database.

9.1.2 CT status

On the left side of the CT Commissioning module, there is a list of the CTs available in the machine database. There are three types of CTs:

- **Commissioned machines** – CTs at the user clinic which are ready for treatment. Commissioned CTs cannot be edited.
- **Uncommissioned machines** – CTs at the user clinic where the editing has not yet been completed. Uncommissioned machines can be edited.
- **Deprecated machines** – previously commissioned CTs that are no longer eligible for plan generation. It is not possible to re-compute doses calculated with a deprecated CT. Deprecated CTs cannot be edited.

9.2 OPERATIONS ON CTS

Right-clicking on a CT name will give access to a few alternatives. For a commissioned, uncommissioned or deprecated CT:

- **Copy** – copies the CT to the uncommissioned machines, allowing the user to edit the machine properties.

Additional alternatives for an uncommissioned CT:

- **Commission** – moves the uncommissioned machine to the commissioned machines, making it impossible to edit the machine and making the machine eligible for clinical planning and dose computation. The step is password protected.
- **Delete** – deletes the CT from the machine database.

Additional alternative for a commissioned machine:

- **Deprecate** – moves the CT to the deprecated machines.

When creating a new version of a CT machine, that is deprecating a commissioned CT and creating a new commissioned CT with the same name, the deprecated CT machine will no longer be available in RayStation. When opening a patient mapped to the deprecated machine, the user will be notified that there exists a newer version of the machine. It will be possible to review old doses calculated based on the deprecated machine but it will not be possible to calculate new dose without updating to the new machine version. Updating to the new version will invalidate calculated doses.

9.3 THE CT COMMISSIONING MODULE WORKSPACE

A CT machine can be used for planning; densities are extracted using the HU-to-density table. CBCT machines are used for dose tracking; density conversions are defined for each image set individually.

In this section

This section contains the following sub-sections:

9.3.1	CT name	p. 359
9.3.2	Commissioning data	p. 360
9.3.3	Type of machine – CT	p. 361
9.3.4	Type of machine – CBCT	p. 362
9.3.5	CT-to-density table	p. 363

9.3.1 CT name

The CT name can be no longer than 81 characters and the name must be unique for all commissioned or uncommissioned CT-machines. Deprecated CTs keep the name they had when commissioned, otherwise there are no restrictions on unique names for deprecated CTs.

Note: *For automatic mapping of a CT-dataset to a specific CT during DICOM import, use the same name for the CT as used in the DICOM-data tag [Station name; 0008,1010]. In order to use different CT to density tables for different protocols, use the name convention StationName:ProtocolName, where protocol name corresponds to the DICOM-data tag [Protocol name; 0018,1030]. CT machine version information is not available in DICOM, mapping will be done to the latest machine version with that name.*

9.3.2 Commissioning data

The name of the user performing the commissioning and the time at commissioning is shown for commissioned and deprecated CTs.

Figure 184. CT commissioning data.

9.3.3 Type of machine – CT

A commissioned CT-model can be used for treatment planning and dose computation. That means that the Hounsfield Units-to-density table and the graph interpolation shown in the CT-to-density graph are used to convert the Hounsfield Units (HU) of the CT-images to mass densities (*section 9.3.5 CT-to-density table on page 363*).

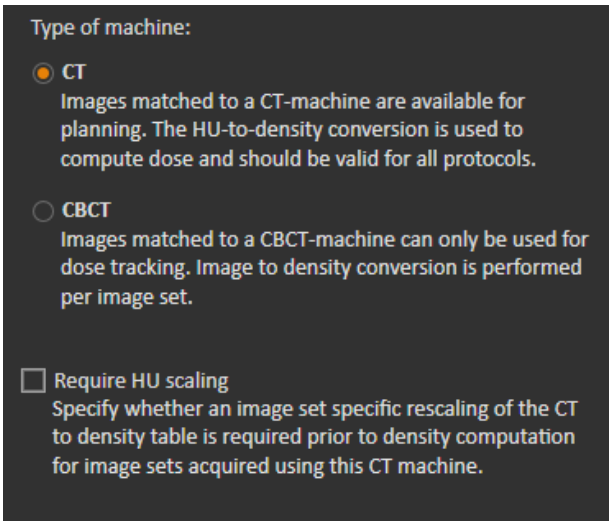
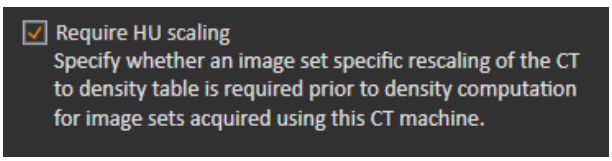

Type of machine:
CT
Images matched to a CT-machine are available for planning. The HU-to-density conversion is used to compute dose and should be valid for all protocols.
CBCT
Images matched to a CBCT-machine can only be used for dose tracking. Image to density conversion is performed per image set.
Require HU scaling
Specify whether an image set specific rescaling of the CT to density table is required prior to density computation for image sets acquired using this CT machine.

Figure 185. The Type of machine information field with CT selected.

HU scaling

For CT machines it is possible to specify whether an image specific calibration, HU scaling, of the CT to density table is required before density computation. This calibration is made in the Image Set Properties dialog in the Patient Data Management module in RayStation.


Require HU scaling
Specify whether an image set specific rescaling of the CT to density table is required prior to density computation for image sets acquired using this CT machine.

9.3.4 Type of machine – CBCT

A commissioned CBCT-model can be used for dose tracking. Image density conversions are defined for each image set individually.

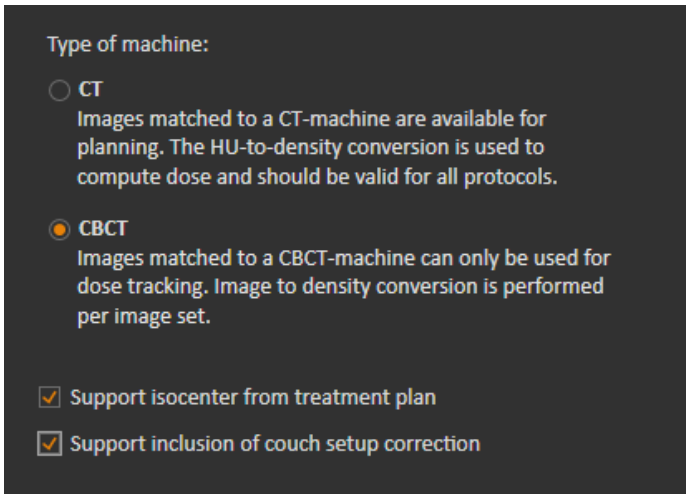

Type of machine:
CT
Images matched to a CT-machine are available for planning. The HU-to-density conversion is used to compute dose and should be valid for all protocols.
CBCT
Images matched to a CBCT-machine can only be used for dose tracking. Image to density conversion is performed per image set.
Support isocenter from treatment plan
Support inclusion of couch setup correction

Figure 186. The Type of machine information field with CBCT selected.

CBCT parameters

There are two CBCT-parameters:

- Support isocenter from treatment plan
- Support inclusion of couch setup correction

9.3.5 CT-to-density table

When computing dose, the HU of the CT-images are converted to mass densities using linear interpolation, as visualized in the CT to density graph. HU values smaller than the lowest HU are given the same density as the lowest HU. HU values larger than the largest HU are given the same density as the largest HU. The densities are not allowed to decrease with HU.

Delete an entry by selecting it in the table and clicking **Delete**. Add a new entry by editing the boxes below the table and click **Add/Edit**. Change the Mass density for an HU by marking the row in the table and editing the Mass density in the box below the table, then click **Add/Edit**. Note that marking a row, changing the HU and clicking **Add/Edit** creates a new entry, and does not delete the original entry.

HU to mass density values can also be imported in a .csv format created in excel where the first column is the HU and the second is the mass density.

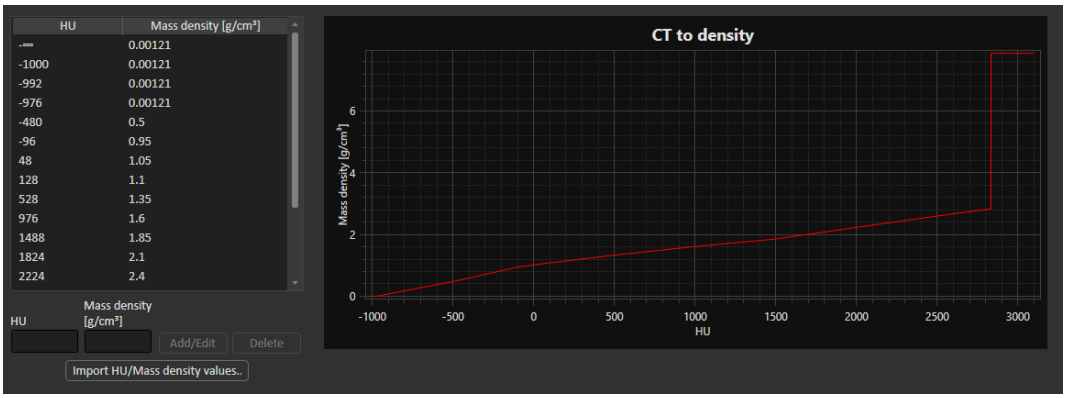
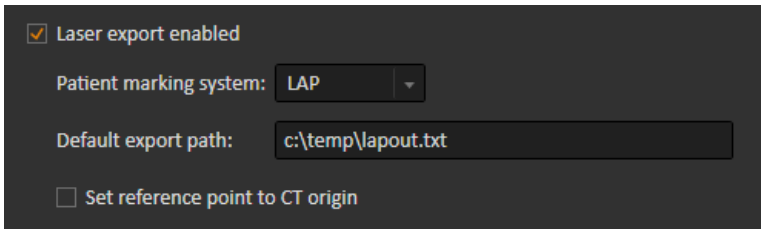


Figure 187. The CT to density table.

9.4 ENABLE LASER EXPORT

If laser export is going to be used in the Virtual Simulation module in RayStation, this has to be enabled.



1. Enable laser export by checking the **Laser export enabled** checkbox.
2. Select **Patient marking system**.
3. Select **Default export path**.
4. Select to **Set reference point to CT origin** by checking the corresponding checkbox.

A MACHINE BACKUP AND RESTORE

The backup and restore functionality is primarily designed for communicating data between the clinic and RaySearch, e.g., if there are problems related to a specific data set. It will not be possible to restore a machine backed up in one RayPhysics version, with an earlier version of RayPhysics. This functionality should not be used for long-term storage of beam data. It is useful for backups in the current version, however.

Only treatment machines can be backed up and restore, it is not possible to backup and restore CT machines in the RayPhysics application. It is however possible to backup and restore CT machines together with patients in the main RayStation application.

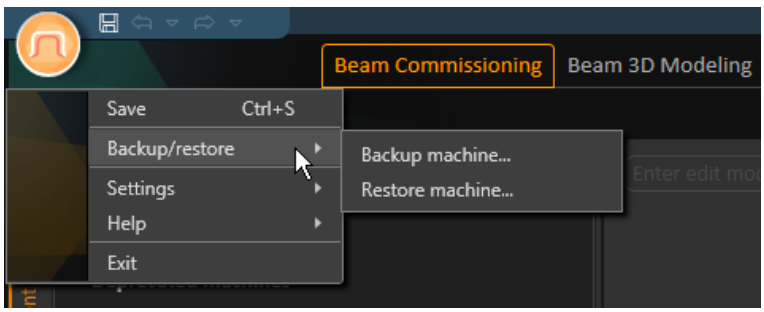


Figure 188. **Backup machine** and **Restore machine** are both found in the RayPhysics drop-down menu.

Note: *Backup and restore can only be done in the Beam Commissioning module or in the CT Commissioning module.*

Note: *When restoring a treatment machine or a CT machine together with a patient, it will not be accessible in the machine tree in RayPhysics in an already open instance of the application. The RayPhysics application has to be restarted or the user can enter the Beam Commissioning module and click the Refresh machine list button in order to display the restored CT machine.*

A.1 BACKUP MACHINE

A machine backup can be exported as a .rsbak file. This file is checksum protected, meaning that it cannot be imported if it has been edited.

1. Select **Backup/Restore** from the RayPhysics menu and **Backup machine...**. This opens the Backup machine dialog.

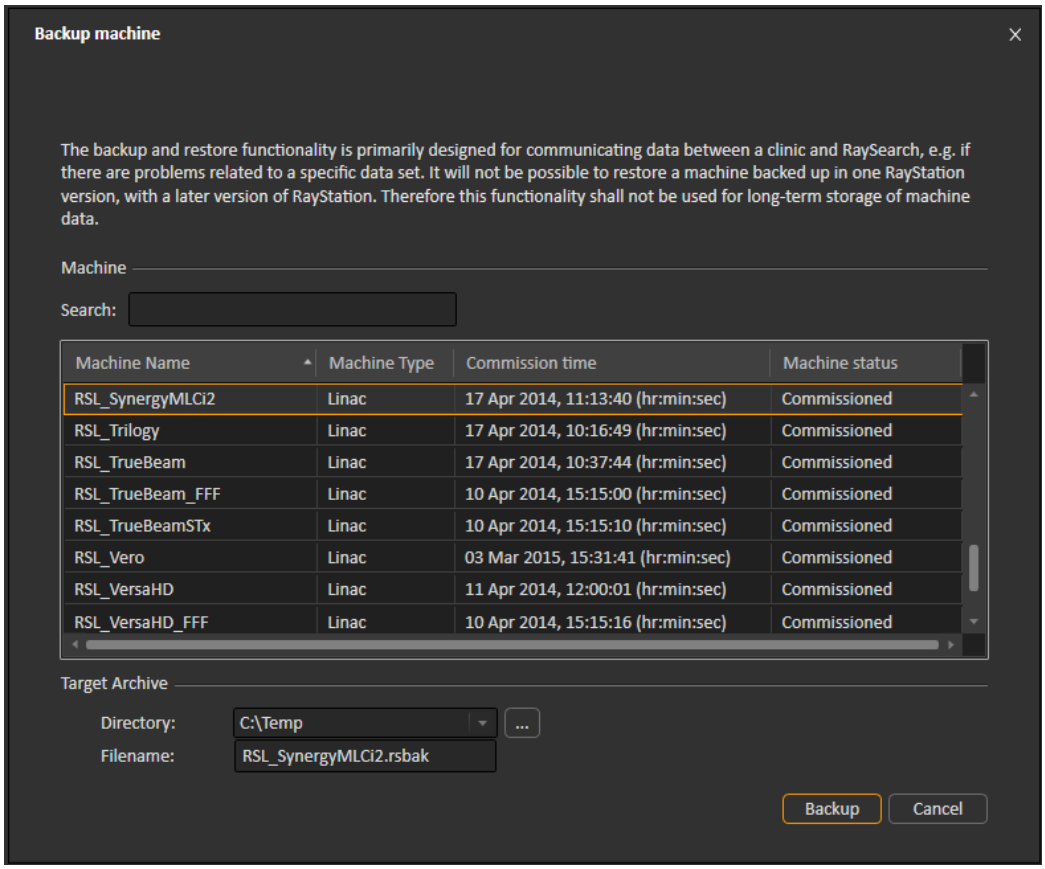

Backup machine
The backup and restore functionality is primarily designed for communicating data between a clinic and RaySearch, e.g. if there are problems related to a specific data set. It will not be possible to restore a machine backed up in one RayStation version, with a later version of RayStation. Therefore this functionality shall not be used for long-term storage of machine data.
Machine
Search:
Machine Name
Machine Type
Commission time
Machine status
RSL_SynergyMLCi2 Linac 17 Apr 2014, 11:13:40 (hr:min:sec) Commissioned
RSL_Trilogy Linac 17 Apr 2014, 10:16:49 (hr:min:sec) Commissioned
RSL_TrueBeam Linac 17 Apr 2014, 10:37:44 (hr:min:sec) Commissioned
RSL_TrueBeam_FFF Linac 10 Apr 2014, 15:15:00 (hr:min:sec) Commissioned
RSL_TrueBeamSTx Linac 10 Apr 2014, 15:15:10 (hr:min:sec) Commissioned
RSL_Vero Linac 03 Mar 2015, 15:31:41 (hr:min:sec) Commissioned
RSL_VersaHD Linac 11 Apr 2014, 12:00:01 (hr:min:sec) Commissioned
RSL_VersaHD_FFF Linac 10 Apr 2014, 15:15:16 (hr:min:sec) Commissioned
Target Archive
Directory:
C:\Temp
...
Filename:
RSL_SynergyMLCi2.rsbak
Backup
Cancel

Figure 189. The Backup machine dialog.

2. Select a machine in the list by clicking on it.
3. Select a **Directory** for the machine in the database.
4. Click **Backup**.

A.2 RESTORE MACHINE

All .rsbak files with machine models can be imported only if they are created with the same or earlier versions of RayStation, and have not been changed manually between export and import.

If a commissioned, un-commissioned or template machine with the same name is present the machine cannot be restored without changing the name at import. This is done automatically by RayPhysics, a suffix will be added at the end of the machine name, e.g., "_1". The name must also be changed at import if both the name and the commissioning date are identical to those belonging to a deprecated machine. If both name and commissioning time is identical for a commissioned machine, restore will not be allowed. To restore a machine, the correct user password in the authentication dialog must be entered.

Note: *The commissioning status of the machines is kept at rsbak restore. Restoring a commissioned machine will directly make the machine available for plan generation in RayStation.*

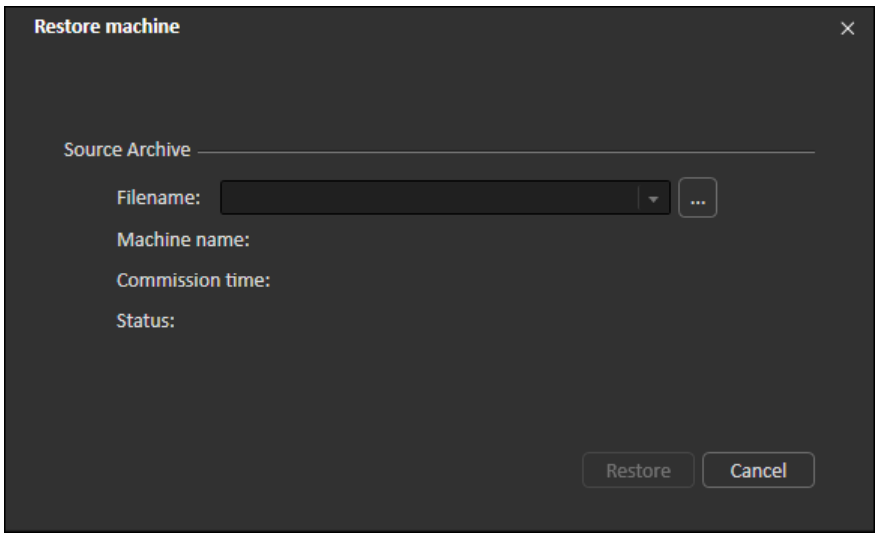


Figure 190. The Restore machine dialog.

A.2.1 Restore and deprecate proton machine

For proton machines, the user has the possibility to deprecate the existing machines directly from the restore dialog by checking the **Deprecate** checkbox.

If the .rsbak file is a newer version of an existing machine and is intended to replace the existing machine, check the **Deprecate** box, the exiting machine will be deprecated and the new will be restored. Otherwise, the new machine will be renamed with a suffix.

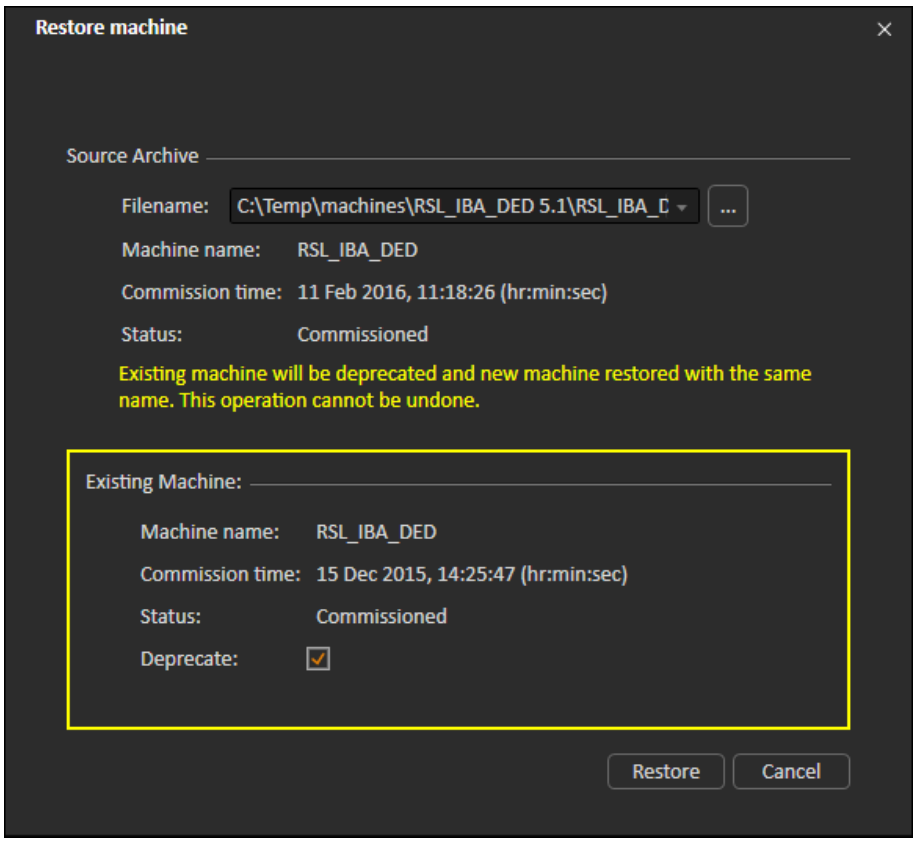


Figure 191. Restore and deprecate proton machine.

B DOSE CURVE FORMAT

In this chapter

This chapter contains the following sections:

B.1	Dose curveformatRFA (.asc) Dose curve format	p. 370
B.2	Comma-separated values (.csv) Dose curve format	p. 375
B.3	Sun Nuclear (.snctxt) Dose curve format	p. 389
B.4	MEPHYSTO (.MCC) Dose curve format	p. 400

B.1 RFA (.ASC) DOSE CURVE FORMAT

In this section

This section contains the following sub-sections:

B.1.1	General	p. 371
B.1.2	Structure	p. 372
B.1.3	Example	p. 373

B.1.1 General

- asc files can be exported using OmniPRO Accept (IBA Dosimetry GmbH).
- .asc files may be opened using Notepad.
- Only " . " is supported as decimal separator.
- Several measurement scans can be stored in the same file.

Each line will start with a character, defining the type of information:

- " : " = Separation between dumped measurements
- " # " = Comment, skip this text altogether
- " %xyz " = Label information, xyz defines type of info to follow
- " ! " = Operator comment in label
- " = " = Measurement data
- The x, y and z coordinates are read from .asc files with the following mapping: XRFA=-YIEC, YRFA=XIEC, and ZRFA=-ZIEC (=Depth), where the subscript IEC refers to IEC61217 standard for the gantry coordinate system. It is assumed that given coordinates are absolute and not relative to the starting point.

Note: *Due to the differences in the RFA and IEC coordinate systems, please make sure that your cross- and inline measurements really corresponds to the crossline (X) and inline (Y) dose curves displayed.*

Note: *Curve orientation and position are read from the start scan value (STS) and the stop scan value (ENDS) in the .rfa/.asc-file. For x-, y- and diagonal profiles, the depth is read from the dose point list and for x-profiles the offset is read from the point list. Note that for y-profiles, all x-coordinates in the dose point list need to be zero.*

B.1.2 Structure

```
%TYP value # TYPE value: UDF = UNDEFINED | SCN 1.0 = SCAN (SCAN STEP (MM))
   | ISO 0.5 = ISODOSE (ISO STEP (MM))

%FSZ 10 10 # FIELDSIZE (MM * MM)

%BMT value # BEAMTYPE value: UDF = UNDEFINED | ELE 6.0 = ELECTRONS (MEV) |
   PHO 6.0 = PHOTONS (MV) | COB = COBALT | CES = CESIUM | RAD = RADIUM |
   OTH = OTHER

%SSD 1000 # SSD (MM)

%STS 0.0 0.0 0.0 # Start Scan X Y Z (MM)

%EDS 0.0 0.0 -10 # End Scan X Y Z (MM )

= X Y Z Dose # Measurement point

:EOM # End of Measurement

:EOF # End of File
```

Beam Commissioning Limitations

Only TYP: **SCN** is supported.

Diagonal profiles are only supported for photons. Diagonal profiles must cross the central axis.

B.1.3 Example

```
:MSR 1 # No. of measurement in file
:SYS BDS 0 # Beam Data Scanner System
#
# RFA300 ASCII Measurement Dump (BDS format)
#
# Measurement number 1
#
%VNR 1.0
%MOD
%TYP SCN
%SCN DPT
%FLD ION
%DAT 01-25-2007
%TIM 15:50:25
%FSZ 50 50
%BMT PHO 6.0
%SSD 900
%BUP 0
%BRD 1000
%FSH -1
%ASC 0
%WEG 0
%GPO 0
%CPO 0
%MEA 1
%PRD 0
%PTS 801
%STS 0.0 0.0 400.2 # Start Scan values in mm ( X , Y , Z )
%EDS 0.0 0.0 393.2 # End Scan values in mm ( X , Y , Z )
! Dataset electronen BlauwSli
!
#
# X Y Z Dose
#
= 0.0 0.0 400.2 17.8
= 0.0 0.0 399.7 17.8
= 0.0 0.0 399.2 17.8
```

```
= 0.0 0.0 398.7 18.0
= 0.0 0.0 398.2 18.0
= 0.0 0.0 397.7 18.0
= 0.0 0.0 397.2 18.0
= 0.0 0.0 396.7 18.0
= 0.0 0.0 396.2 18.2
= 0.0 0.0 395.7 18.3
= 0.0 0.0 395.2 18.2
= 0.0 0.0 394.7 18.2
= 0.0 0.0 394.2 18.3
= 0.0 0.0 393.7 18.3
= 0.0 0.0 393.2 18.3
:EOM # End of Measurement
:EOF # End of File
```

B.2 COMMA-SEPARATED VALUES (.CSV) DOSE CURVE FORMAT

In this section

This section contains the following sub-sections:

B.2.1	General	p. 376
B.2.2	Diagonal curves	p. 378
B.2.3	Structure	p. 380
B.2.4	LINAC treatment machines	p. 382
B.2.5	Ion treatment machines	p. 386

B.2.1 General

- .csv files is an ascii-type export of a one-sheet Microsoft Office Excel file. The example file is shown in ascii.
- ";" is used as value separator.
- White space and case are disregarded.
- Each item is one line.
- Line end is Windows (CR/LF).
- Literals are in bold.
- Only "." is supported as decimal separator. Note that there may be problems importing *.csv files if "," is selected as decimal symbol instead of "." under Windows Region and Language settings.
- Several measurement scans can be stored in the same file.
- The coordinate system used, is a left-handed system with the X- and Y-axes in accordance with the IEC61217 standard for the gantry coordinate system. The Z-axis is along the depth axis, indicating the depth from the surface downwards, i.e. in the opposite direction from the Z-axis in the IEC61217 standard.
- There are four different dose curve types : Depth, Crossline, Inline and Diagonal. The Depth curve is measured along the Z-axis, the Crossline curve along the X-axis, and the Inline curve along the Y-axis. Diagonal curves may have different orientations, see *section B.2.2 Diagonal curves on page 378*. Diagonal curves are only supported for photons and must cross the central axis.
- The field size must be reflection symmetric around the depth axis (X=0, Y=0).
- The start point must be on the central axis (X=0, Y=0) for depth dose curves. For dose profiles (Crossline, Inline and Diagonal curves), the Z-point is read from the three coordinates in the start point specification; it indicates the depth from the surface downwards. For depth dose curves, the Z coordinate of the start point specification must be equal to 0, since it is assumed that given coordinates along the profile are absolute and not relative to the starting point.
- The csv format accepts the tags WedgeType and WedgeAngle for wedged curves. The following wedge types are supported: ElektaMotorized, Standard, EDW, and SiemensVirtual. If the wedge type and angle is allowed by the machine, the dose curves will automatically be imported to the wedge type specified in the file.
- If the dose curve type is Diagonal, the tag DiagonalAngle must be given specifying the angle of the diagonal profile. See *section B.2.2 Diagonal curves on page 378* for more information.
- Rows prefixed with the "#" symbol are ignored during import.
- For photon beam qualities: if the tag FluenceMode is written in the dose curve file, the fluence mode in the file is checked against the fluence mode of the beam quality.

The data set consists of two columns. In the first column, depending on curve type, one of the coordinates X, Y or Z is given, and in the second column, the dose is given. For diagonal curves, the first column is interpreted as a radius coordinate. See *section B.2.2 Diagonal curves on page 378* for more information. The coordinate system is described in *section 2.3.8 Dose curve coordinate system in RayPhysics on page 43*.

B.2.2 Diagonal curves

The orientation of a diagonal curve is given by the DiagonalAngle tag, which can have angles between 0° and 360°. The diagonal angle is defined according to:

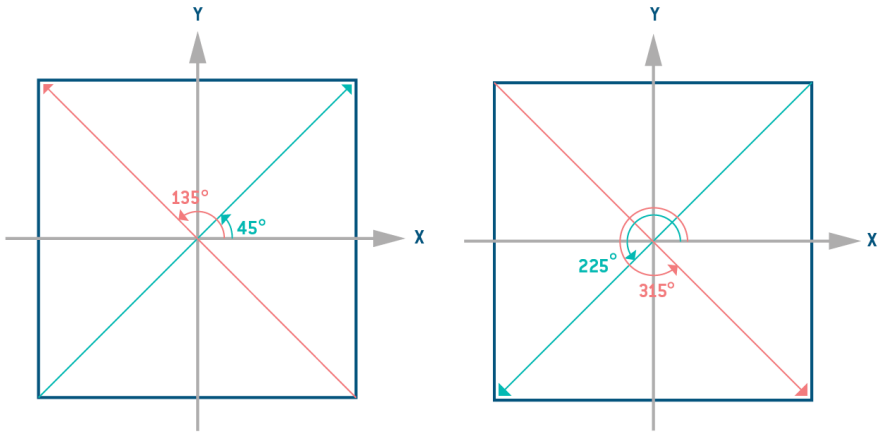


Figure 192. Angle definitions for diagonal angle tag

The measuring point is interpreted as a radius position and the x and y positions are calculated from:

$$x = radius \times \cos\Theta$$
$$y = radius \times \sin\Theta$$

[Eq. 18]

where Θ is the diagonal angle in radians.

Example:

Measuring position/radius	Diagonal angle (degrees)	RayPhysics x-coordinate	RayPhysics y-coordinate
-10.0	45	-7.07	-7.07
-5.0	45	-3.54	-3.54
0.0	45	0.0	0.0
2.0	45	1.41	1.41
4.0	45	2.83	2.83
8.0	45	5.66	5.66
-10.0	315	-7.07	7.07
-5.0	315	-3.54	3.54

Measuring position/radius	Diagonal angle (degrees)	RayPhysics x-coordinate	RayPhysics y-coordinate
0.0	315	0.0	0.0
2.0	315	1.41	-1.41
4.0	315	2.83	-2.83
8.0	315	5.66	-5.66
-10.0	120	5.0	-8.66
-5.0	120	2.5	-4.33
0.0	120	0.0	0.0
2.0	120	-1.0	1.73
4.0	120	-2.0	3.46
8.0	120	-4.0	6.93

B.2.3 Structure

```
EnergySpecification := energy[MV]: SepChar IntegerValue
SourceSurfaceDistanceSpecification := SSD[mm]: SepChar DoubleValue
FieldSizeSpecification1 := Fieldsize[mm]: SepChar X1 SepChar Y1
SepChar X2 SepChar Y2
X1 := DoubleValue
Y1 := DoubleValue
X2 := DoubleValue
Y2 := DoubleValue
ConeNameSpecification := ConeName: SepChar StringValue
WedgeTypeSpecification := WedgeType: SepChar WedgeTypeEnumerator
WedgeTypeEnumerator := ElektaMotorized | Standard | EDW | SiemensVirtual
WedgeAngleSpecification := WedgeAngle[deg]: SepChar DoubleValue
ApplicatorSpecification := Applicator: SepChar ApplicatorTypeEnumerator
   X1xX2
X1 := DoubleValue
X2 := DoubleValue
ApplicatorTypeEnumerator := Elekta | Varian | Siemens
CurveTypeSpecification := CurveType: SepChar CurveTypeEnumerator
CurveTypeEnumerator := Depth | Inline | Crossline | Diagonal
DiagonalAngleSpecification := DiagonalAngle[deg] : SepChar DoubleValue
RadiationTypeSpecification := RadiationType: SepChar
RadiationTypeEnumerator
RadiationTypeEnumerator := Photon | Electron
FluenceModeSpecification := FluenceMode: SepChar FluenceModeEnumerator
FluenceModeEnumerator := Standard | FFF | SRS
MediumSpecification := Medium: SepChar MediumEnumerator
MediumEnumerator := Water|Air
QuantitySpecification := Quantity: SepChar QuantityEnumerator
QuantityEnumerator := RelativeDose | AbsoluteDose
StartPointSpecification2 := StartPoint[mm]: SepChar X SepChar Y SepChar Z
X := DoubleValue
Y := DoubleValue
Z := DoubleValue
PointList := { MeasuredPoint }+
MeasuredPoint := { Distance SepChar MeasurementValue}+
Distance := DoubleValue
MeasurementValue := DoubleValue
EndTag := End
```

Note: *The EnergySpecification entry in the case of electrons is given by the tag energy[MeV], instead of energy[MV].*

Beam Commissioning Limitations

Only Quantity: RelativeDose is supported.

Diagonal profiles are only supported for photons. Diagonal profiles must cross the central axis.

B.2.4 LINAC treatment machines

Example: Open photon curve

```
energy[MV]:; 6
SSD[mm]:; 1000
Fieldsize[mm]:; -15; -15; 15; 15;
CurveType:; Depth
RadiationType:; Photon
FluenceMode:; Standard
Quantity:; RelativeDose
StartPoint[mm]:; 0; 0; 0
0.0; 43.420
5.0; 78.330
10.0; 96.840
15.0; 99.740
20.0; 97.340
25.0; 95.240
30.0; 93.140
35.0; 90.240
40.0; 87.540
45.0; 84.640
50.0; 82.340
55.0; 79.740
60.0; 77.830
End
```

Example: Diagonal profile with diagonal angle 45 degrees

```
energy[MV]:; 6
SSD[mm]:; 1000
Fieldsize[mm]:; -200; -200; -200; -200;
CurveType:; Diagonal
RadiationType:; Photon
DiagonalAngle[deg]:; 45
Quantity:; RelativeDose
StartPoint[mm]:; -14.48; -14.48; 15
-20.48; 3.3209
-17.92; 3.3196
-15.36; 3.3031
-12.80; 3.2959
```

```
-10.24; 3.2877
-7.68; 3.2832
-5.12; 3.2832
-2.56; 3.2740
0.00; 3.2829
2.56; 3.2777
5.12; 3.2774
7.68; 3.2842
10.24; 3.2880
12.80; 3.2901
15.36; 3.3031
17.92; 3.3103
20.48; 3.3266
23.04; 3.3405
End
```

Example: Wedged photon curve for Standard wedge with wedge angle 15 degrees

```
energy[MV]:; 6
SSD[mm]:; 1000
Fieldsize[mm]:; -15; -15; 15; 15;
WedgeType:; Standard
WedgeAngle[deg]:; 15
CurveType:; Depth
RadiationType:; Photon
FluenceMode:; Standard
Quantity:; RelativeDose
StartPoint[mm]:; 0; 0; 0
0.0; 43.420
5.0; 78.330
10.0; 96.840
15.0; 99.740
20.0; 97.340
25.0; 95.240
30.0; 93.140
35.0; 90.240
40.0; 87.540
45.0; 84.640
50.0; 82.340
55.0; 79.740
```

```
60.0; 77.830
End
```

Example: Photon cone curve

```
energy[MV]:; 6
SSD[mm]:; 1000
Fieldsize[mm]:; -3; -3; 3; 3
ConeName:; Cone6
CurveType:; Crossline
RadiationType:; Photon
FluenceMode:; Standard
Quantity:; RelativeDose
StartPoint[mm]:; -25.3210714285714; 0; 149.7
-25.3; 0.265
-25.1; 0.265
-24.9; 0.265
-24.6; 0.265
-24.4; 0.265
-24.1; 0.265
-23.9; 0.265
-23.6; 0.265
-23.4; 0.265
-23.2; 0.265
-23.0; 0.265
-22.9; 0.265
-22.8; 0.265
-22.5; 0.265
-22.4; 0.265
-22.2; 0.265
-22.0; 0.265
End
```

Example: Electron applicator depth curve

```
energy[MeV]:; 6
SSD[mm]:; 1000
Fieldsize[mm]:; -15; -15; 15; 15;
Applicator:; Elekta 6x6
CurveType:; Depth
RadiationType:; Electron
Medium: Water
```

```
Quantity:; RelativeDose
StartPoint[mm]:; 0; 0; 0
0.0; 43.420
5.0; 78.330
10.0; 96.840
15.0; 99.740
20.0; 97.340
25.0; 95.240
30.0; 93.140
35.0; 90.240
40.0; 87.540
45.0; 84.640
50.0; 82.340
55.0; 79.740
60.0; 77.830
End
```

B.2.5 Ion treatment machines

File formats for Ion treatment machines

This section describes the required file format and required measurement data for beam modeling data import in RayPhysics. Use one file for each type of measurement (Pristine Bragg peaks, Spot profiles and Absolute dosimetry) and use the file format as described in this section.

The file name is not used, but the file ending/format should be .csv.

Data format: Delimiters can be semicolon (;) or comma (,). Lines starting with hash symbol (#) indicates comment and will not be read.

Pristine Bragg peaks

```
Origin of data [Measured/Computed]:; Measured
Machine/Treatment room:;
Snout name:;
Radiation type:; Proton
Curve type [Depth/X/Y/AbsoluteDosimetry]:; Depth
Medium:; Water
Single spot [Yes/No]:;
Scanned field size (x y) [mm]:; Defined by the positions at the isocenter
   of the centers of the outermost spots/lines. Only needs to be specified
   if Single spot = No
Spot spacing [mm]:; Only needs to be specified if Single spot = No
Isocenter to snout distance [mm]:; Refers to the snout position, i.e., the
   isocenter to snout position plane distance.
Isocenter to phantom surface distance [mm]:; Refers to the distance between
   the water phantom surface and the isocenter.
Detector lateral shape [Quadratic/Circular]:;
Detector lateral side/diameter [mm]:;
Nominal beam energy [MeV]:;
Measured dose curve (Depth [mm] Dose [a.u.]):;
depth1; d1
..
depthN; d1
End:;
```

Spot profiles

```
Origin of data [Measured/Computed]:; Measured
Machine/Treatment room:;
Snout name:;
Radiation type:; Proton
Curve type [Depth/X/Y/AbsoluteDosimetry]:; X or Y
Medium:; Air
```

```
Single spot [Yes/No]:; Yes

Isocenter to snout distance [mm]:; Refers to the snout position, i.e., the
   isocenter to snout position plane distance.

Air profile Z pos [mm]:; Position of the measurement plane on the central
   beam axis (IEC gantry Z axis). Positive Z values are upstream (closer
   to the source) of negative Z values in the IEC gantry coordinate system.

Nominal beam energy [MeV]:;

Measured fluence curve (X pos [mm] Y pos [mm] Fluence [a.u.]):;

x1; y1; f1

…

xN; yN; fN;

End:;
```

Absolute dosimetry for PBS machines

```
Origin of data [Measured/Computed]:; Measured

Machine/Treatment room:;

Snout name:;

Radiation type:; Proton

Curve type [Depth/X/Y/AbsoluteDosimetry]:; AbsoluteDosimetry

Medium:; Water

Isocenter to snout distance [mm]:; Refers to the snout position, i.e., the
   isocenter to snout position plane distance.

Scanned field size (x y) [mm]:; Defined by the positions at the isocenter
   of the centers of the outermost spots/lines.

Spot spacing [mm]:;

Detector lateral shape [Quadratic/Circular]:; Optional. A generic detector
   is assigned at import if detector properties are not specified in the
   file.

Detector lateral side/diameter [mm]:;

Measurement (Nominal energy [MeV] Depth [mm] Isocenter to phantom surface
   distance [mm] DosePerMU [cGy/MU]):;

e1; d1; isd1; dpmu1

…

eN; dN; isdN; dpmuN

End:;
```

Note: *For machines with NP instead of MU, "DosePerMU [cGy/MU]" is replaced by "DosePerMeterset [cGy/NP]"*

Absolute dosimetry for Line Scanning machines

```
Origin of data [Measured/Computed]:; Measured

Machine/Treatment room:;

Snout name:;

Radiation type:; Proton
```

```
Curve type [Depth/X/Y/AbsoluteDosimetry]:; AbsoluteDosimetry

Medium:; Water

Isocenter to snout distance [mm]:; Refers to the snout position, i.e., the
   isocenter to snout position plane distance.

Scanned field size (x y) [mm]:; Defined by the positions at the isocenter
   of the centers of the outermost spots/lines.

Spot spacing [mm]:;

Detector lateral shape [Quadratic/Circular]:; Optional. A generic detector
   is assigned at import if detector properties are not specified in the
   file.

Detector lateral side/diameter [mm]:;

Measurement (Nominal energy [MeV] Depth [mm] Isocenter to phantom surface
   distance [mm] Meterset [MU] DosePerMU [cGy/MU]):;

e1; d1; isd1; ms1; dpmu1

…

eN; dN; isdN; msN; dpmuN

…

End:;
```

B.3 SUN NUCLEAR (.SNCTXT) DOSE CURVE FORMAT

In this section

This section contains the following sub-sections:

B.3.1	General	p. 390
B.3.2	Structure	p. 391
B.3.3	Example	p. 396

B.3.1 General

The file is an ASCII file that can be opened and manipulated in any text editor.

The file contains three columns of data which are separated by a TAB character represented by: **\t**. The first column contains the key for each line, the second column contains the value for each line and the third column supports comments for each line (optional).

An example of a line in the ASCII file: File Name**\t**example.snctxt**\t**Name of the file,

where:

Key	Value	Comments (optional)
File Name	example.snctxt	Name of the file

Each property should be contained in a single line. To support multiline data in the Scan Comments property, there is a convention used to replace any CRLF characters with <newline>. Upon import, the <newline> characters are replaced with CRLF.

The beginning of the file contains a file header that shows general information regarding the file. The file may contain one or more scans. For each scan, there are several sections which include scan header, the dose table and the optional raw data. The scan header is not contiguous at the start of the scan. Instead it is broken into two sections separated by the dose table.

Note: *Curve orientation is read from the Scan Type in the .snctxt-file. For x-, y- and diagonal profiles, the depth is read from the Dose table and for x-profiles the offset is read from the Dose table. Note that for y-profiles, all x-coordinates in the Dose table need to be zero.*

B.3.2 Structure

File header

In the beginning of each file there is a file header. The file header consists of the following information:

Key	Description
Tab-Delimited Scan Output	File format identifier
File Name	Name of current file
File Date	Date file was generated
File Version	Version of the SNCTXT file format specification 2.0 or greater
File Export Version	Version of SNC Dosimetry software used to generate file
File Scan Count	Number of scans included in file

```
Tab-Delimited Scan Output
FILE HEADER
File Name example.snctxt
File Date 01/10/2012 09:32
File Export Version 1.4.0.34714
File Version 2.0
File Scan Count 1
```

Scan data

Each scan in the file has its own scan header. The scan header contains all the characteristics of a scan from energy and field size to equipment serial numbers and revisions. The start of the scan is indicated by the key **BEGIN SCAN** and the end is indicated by **END SCAN**. The exact values contained in the scan header are dependent on the scan properties. The organization of the properties in the file is based on categories (Summary, Equipment, Delivery System, etc.). The exact order of the properties is not absolute and is open to change.

Below is a list of all possible scan properties:

Key	Description
BEGIN SCAN	
Summary Comments	Scan comments
Summary Beam Type	Type of energy (Photon or Electron)
Summary Energy (MV/MeV)	Magnitude of the energy
Summary Field Size X (cm)	Field size

Key	Description
Summary Field Size Y (cm)	Field size
Summary Wedge Angle (degrees)	Angle of the wedge
Summary Wedge Direction	Wedge direction (In, Out, Left, Right)
Summary Scan Type	Type of scan (Inline, Crossline, Depth Scan, Profile at Angle, Point Measurement, Point to Point, Ray Trace)
SCAN HEADER	
FACILITY INFORMATION	
Institution	Name of institution
Delivery System	Name of delivery system
Delivery System Manufacturer	Manufacturer of delivery system
Delivery System Model #	Delivery system model
Delivery System Serial #	Delivery system serial number
Field Detector Model #	Model of field detector
Field Detector Serial #	Serial number of field detector
Reference Detector Model #	Model of reference detector
Reference Detector Serial #	Serial number of reference detector
SNC EQUIPMENT	
Application Programming Interface	Version of SNCAPI.dll
Hardware Device Interface	Version of SunNuclear.Device.Interface.dll
3D Scanner Model #	Water tank model
3D Scanner Serial #	Water tank serial number
3D Scanner Firmware	Firmware version of water tank electronics
Drive Factor Diameter (pulse/mm)	Diameter drive factor
Drive Factor Vertical (pulse/mm)	Depth drive factor
Drive Factor Ring (pulse/mm)	Ring drive factor
Electrometer Model #	Electrometer model
Electrometer Serial #	Electrometer serial number
Electrometer Firmware	Firmware version of electrometer

Key	Description
Leveling Platform Model #	Leveling platform model
Leveling Platform Serial #	Leveling platform serial number
Lift Table Model #	Lift table model
Lift Table Serial #	Lift table serial number
Reservoir Model #	Reservoir model
Reservoir Serial #	Reservoir serial number
DELIVERY SYSTEM	
Beam Type	Type of energy (Photon or Electron)
Energy (MV/MeV)	Magnitude of the energy
Gantry Angle (degrees)	Angle of the gantry
Collimator Angle (degrees)	Angle of collimator
Collimation Type	Type of collimation used (Circular Jaws, Fixed Applicator, Jaws, MLC, Jaws and MLC)
Wedge Type	Wedge type (Open, Fixed)
Wedge Angle (degrees)	Angle of the wedge
Wedge Direction	Wedge direction (In, Out, Left, Right)
Field Size X (cm)	Field size
Field Size Y (cm)	Field size
Field Shape	Square or Circle
Measurement Unit	cm or mm
Collimator Position Jaws X1 (cm)	Jaws X1 position
Collimator Position Jaws X2 (cm)	Jaws X2 position
Collimator Position Jaws Y1 (cm)	Jaws Y1 position
Collimator Position Jaws Y2 (cm)	Jaws Y2 position
Collimator Position MLC X1 (cm)	MLC X1 position
Collimator Position MLC X2 (cm)	MLC X2 position
Collimator Position MLC Y1 (cm)	MLC Y1 position
Collimator Position MLC Y2 (cm)	MLC Y2 position
SETUP PARAMETERS	

Key	Description
Ring Center (cm)	Location of exact center of diameter rail
Angle Offset (degrees)	Angle offset in degrees
Hysteresis Plus (cm)	Measured hysteresis factor
Hysteresis Minus (cm)	Measured hysteresis factor
Ray Trace Crossline Angle (degrees)	Ray trace Auto-Setup crossline angle
Ray Trace Crossline Beam Center (cm)	Ray trace Auto-Setup crossline beam center calculation
Ray Trace Inline Angle (degrees)	Ray trace Auto-Setup inline angle
Ray Trace Inline Beam Center (cm)	Ray trace Auto-Setup inline beam center calculation
Ray Trace Beam Center Depth (cm)	Ray trace Auto-Setup beam center depth
MEASUREMENT DETAILS	
Comments	Scan comments
Scan ID	Unique id of this scan
Scan Date	Date scan was measured
Scan Type	Type of scan (Inline, Crossline, Depth Scan, Profile at Angle, Point Measurement, Point to Point, Ray Trace)
Scan Medium	Location of measurement (Water or Air)
Source to Surface Distance (cm)	Source to Surface Distance (SSD)
Measurement Mode	Movement type (Continuous or Step By Step)
Scan Speed (cm/s)	Speed of continuous movement
Point Spacing (cm)	Distance interval for Step By Step movements
Integration Time (s)	Time interval for Step By Step movements
Duration (s)	Time a point measurement is integrated for
Diameter Drive Scan Direction	Does the scan move in the opposite direction (used for scan optimization)
Half Beam	Is the scan a half beam scan
Additional Scan Range (cm)	Additional scan range beyond field size
Integrated Measurement?	(not used)

Key	Description
Effective Point of Measurement (cm)	Detector position offset from found water level
Detector Bias Voltage (V)	Bias voltage applied to the detectors
Field Background Rate (counts/s)	Background value for the field detector
Reference Background Rate (counts/s)	Background value for the reference detector
Normalization Value (Field/Reference)	Normalization ratio used
Electrometer Temperature (degrees C)	External electrometer sensor temperature reading
Probe Temperature (degrees C)	Internal electrometer sensor temperature reading
Pressure (mbar)	Electrometer air pressure sensor
+5VA Sensor	Electrometer +5VA Sensor reading

Raw data

The raw data is included for each scan if it is available. Raw data is not required. The raw data represents unaltered original information from the electrometer that is acquired during the measurement. Raw data is not read by RayPhysics.

Dose table

The dose table is included for every scan. It describes the data points in the scan as seen in the Dosimetry software.

Below is a list of all possible dose table properties and a description of each:

Key	Description
X (cm)	X coordinate for this data point
Y (cm)	Y coordinate for this data point
Z (cm)	Depth coordinate for this data point
Relative Dose (%)	Relative dose calculated during the scan

Beam commissioning limitations

Only Scan Type Inline, Crossline, Depth Scan and Profile at Angle is supported. Scan Type Profile at Angle (diagonal profile) is only supported for photons. Diagonal profiles must cross the central axis.

B.3.3 Example

```
Tab-Delimited Scan Output
FILE HEADER
File Name example.snctxt
File Date 01/10/2012 09:32
File Export Version 1.4.0.34714
File Version 2.0
File Scan Count 1
BEGIN SCAN
Summary Comments 7 point averaging
Summary Beam Type Photon
Summary Energy (MV/MeV) 6.00
Summary FieldSize X (cm) 4.00
Summary FieldSize Y (cm) 4.00
Summary Wedge Type Open Field
Summary Wedge Angle (degrees) 0.00
Summary Scan Type Crossline
BEGIN DOSE TABLE
Action Initial Scan
X (cm) Y (cm) Z (cm) Relative Dose (%)
-2.065 0 5.002 93.39
-2.022 0 5.002 94.49
-1.98 0 5.002 93.71
-1.938 0 5.002 93.41
-1.896 0 5.002 93.27
-1.854 0 5.002 93.14
-1.812 0 5.002 93.32
-1.77 0 5.002 93.9
-1.728 0 5.002 93.8
-1.686 0 5.002 93.04
-1.644 0 5.002 93.6
-1.602 0 5.002 92.55
-1.56 0 5.002 93.65
-1.517 0 5.002 93.23
-1.475 0 5.002 94.27
-1.433 0 5.002 95.11
-1.391 0 5.002 93.82
-1.349 0 5.002 93.73
```

```
-1.307 0 5.002 92.71
-1.265 0 5.002 93.53
-1.223 0 5.002 94.12
-1.181 0 5.002 93.05
-1.139 0 5.002 95.13
-1.097 0 5.002 93.38
END DOSE TABLE
SCAN HEADER
FACILITY INFORMATION
Institution Sun Nuclear Corporation
Delivery System Research LINAC
Delivery System Manufacturer Varian
Delivery System Model # 2100C
Delivery System Serial # 144
Field Detector Model # LSE
Field Detector Serial #
Reference Detector Model # LSE
Reference Detector Serial #
SNC EQUIPMENT
Application Programming Interface 1.1.11105.1228
Hardware Device Interface 1.0.10328.1435
3D Scanner Model # Not Available
3D Scanner Serial #
3D Scanner Firmware
Drive Factor Diameter (pulse/mm) 1350
Drive Factor Vertical (pulse/mm) 630
Drive Factor Ring (pulse/mm) 706.67
Electrometer Model # Not Available
Electrometer Serial #
Electrometer Firmware
Leveling Platform Model # Not Available
Leveling Platform Serial # Not Available
Lift Table Model # Not Available
Lift Table Serial # Not Available
Reservoir Model # Not Available
Reservoir Serial # Not Available
DELIVERY SYSTEM
Beam Type Photon
Energy (MV / MeV) 6.00
```

```
Gantry Angle (degrees) 0
Collimator Angle (degrees) 0.00
Collimation Type Jaws
Wedge Type Open Field
Wedge Angle (degrees) 0.00
Wedge Direction
Field Size X (cm) 4.00
Field Size Y (cm) 4.00
Collimator Position Jaws X1 (cm)
Collimator Position Jaws X2 (cm)
Collimator Position Jaws Y1 (cm)
Collimator Position Jaws Y2 (cm)
Collimator Position MLC X1 (cm)
Collimator Position MLC X2 (cm)
Collimator Position MLC Y1 (cm)
Collimator Position MLC Y2 (cm)
SETUP PARAMETERS
Ring Center (cm) 25.5
Angle Offset (degrees) 0
Hysteresis Minus (cm) 0
Hysteresis Plus (cm) 0
MEASUREMENT DETAILS
Comments 7 point averaging
Scan Id 1302
Scan Date 05/04/2011 08:27
Scan Type Crossline
Scan Medium Water
Source to Surface Distance (cm) 100.00
Measurement Mode Continuous
Scan Speed (cm/s) 0.1 cm / second
Diameter Drive Scan Direction False
Additional Scan Range (cm) 0.00
Integrated Measurement False
Effective Point of Measurement (cm) 0
Detector Bias Voltage (V) 0.00
Field Background Rate (counts/s) 115.67
Reference Background Rate (counts/s) 136.34
Normalization Value (Field/Reference) 0.921781548353212
Electrometer Temperature (degrees C) 5.754323064239777777777777782
```

```
Probe Temperature (degrees C) 31.934081025406277777777777780
Pressure (mbar) 1034.38917287624000
+5VA Sensor 5.09025096893311
BEGIN RAW DATA
END RAW DATA
END SCAN
```

B.4 MEPHYSTO (.MCC) DOSE CURVE FORMAT

The data format for MEPHYSTO mc² is an ASCII format with extension .mcc. The .mcc file format is used by various PTW software packages and modules. Each line of the file contains a keyword without or with one or more data values. Keywords are only written with uppercase letters. If a data value is expected after a keyword and equals sign (=) separates the keyword from the data value. Between the keyword and the equals sign no space character is allowed. Every line finishes with CR/LF. Apart from this, comment lines are allowed. These lines begin with a quotation mark (').

The data values have no format restrictions: Strings can have any length. An integer value need not have a specific number of digits. Floating point values do not need a specific number of decimals. The data format for MEPHYSTO mc² files consists of a header followed by the description and the measurement values of the scans. Structure of the .mcc file format:

Key name	Description
BEGIN_SCAN_DATA	identifier for the beginning of a MEPHYSTO mc² file
	header information
BEGIN_SCAN 1	identifier for the beginning of a scan 1
	scan description
BEGIN_DATA	identifier for the beginning of the measuring data
	scan data
END_DATA	identifier for the end of the measuring data
END_SCAN 1	identifier for the end of scan 1
BEGIN_SCAN 2	identifier for the beginning of a scan 2
	scan description
BEGIN_DATA	identifier for the beginning of the measuring data
	scan data
END_DATA	identifier for the end of the measuring data
END_SCAN 2	identifier for the end of scan 2
BEGIN_SCAN 3	identifier for the beginning of a scan 3
BEGIN_SCAN 3	identifier for the beginning of a scan 3
…	
END_SCAN	identifier for the end of the last scan
END_SCAN_DATA	identifier for the end of a MEPHYSTO mc² file

For the curve description the following keywords are required (even if there are more possible keywords to describe a curve only the most important ones are explained). Not all dose curves are valid for beam commissioning. The options that are not valid are shown in the table below.

Key name	Data Type	Unit	Description
COMMENT	string		comment
MEAS_DATE	string		measuring date and time
MODALITY	string		modality: X (photons) EL (electrons) Not supported: CO (cobalt) P (protons) N (neutrons) 12C (12 C Ions) HP (heavy particles)
INPLANE_AXIS_DIR	string		direction of the inplane axis GUN_TARGET TARGET_GUN
CROSSPLANE_AXIS_DIR	string		direction of the crossplane axis LEFT_RIGHT RIGHT_LEFT
LINAC	string		LINAC name
ENERGY	float	[MeV] [MV]	energy
SSD	float	[mm]	source detector distance
BLOCK	string		name of the block
WEDGE	string		name of the wedge, required OR name of the applicator for electron curves
WEDGE_ANGLE	Double		wedge angle. Required.
FIELD_INPLANE	float	[mm]	field length in inplane direction
FIELD_CROSSPLANE	float	[mm]	field width in crossplane direction
FIELD_TYPE	string		form of the field: RECTANGULAR Not supported: CIRCULAR IRREGULAR

Key name	Data Type	Unit	Description
GANTRY	float	[°]	gantry angle
GANTRY_UPRIGHT_POSITION	string		definition of the gantry upright position 0 (0 degrees) 180 (180 degrees)
GANTRY_ROTATION	string		rotation direction of the gantry CW (clockwise) CCW (counter clockwise)
COLL_ANGLE	float	[°]	collimator angle
SCAN_CURVETYPE	string		curve type: INPLANE_PROFILE CROSSPLANE_PROFILE PDD Not supported: DDC TPRCURVE OUTPUT_FACTOR
SCAN_DEPTH	float	[mm]	depth of the profile
SCAN_OFFAXIS_INPLANE	float	[mm]	offaxis value in inplane direction ONLY SUPPORT OFFAXIS VAUE = 0
SCAN_OFFAXIS_CROSSPLANE	float	[mm]	offaxis value in crossplane direction ONLY SUPPORT OFFAXIS VALUE = 0
SCAN_ANGLE	float	[°]	measuring angle ONLY SUPPORT ANGLES = 0
SCAN_DIAGONAL	integer		possible values: NOT_DIAGONAL FIRST_DIAGONAL SECOND_DIAGONAL For explanation of these values see *section B.4.5 Diagonal profiles on page 408*.
MEAS_UNIT	string		unit of the measuring data C GY A.U. OD R cGy Gy/min

After the description of the curve the measuring values follow. They have the following format:

```
BEGIN_DATA
Meas. Pos. in [mm] Meas. Value in [MEAS_UNIT] Ref. Meas. Value in [MEAS_UNIT]
   Chamber
... ...
Meas. Pos. in [mm] Meas. Value in [MEAS_UNIT] Ref. Meas. Value in [MEAS_UNIT]
   Chamber
END_DATA
```

All values are separated by a space. The reference measuring values are only available if the measurement was taken against a reference chamber. The chamber number is also not in every measurement available. If there are no reference dose values but chamber numbers, they will be saved directly after the dose values. The chamber numbers are signed with a '#'.

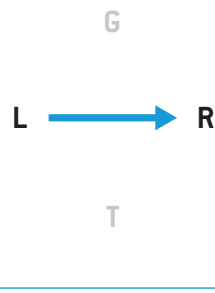
Hints:

- The measuring positions are stored in arrow direction in the scan.
- The data points are transformed to the coordinate system in *section 2.3.8 Dose curve coordinate system in RayPhysics on page 43*, based on the coordinate system definitions of the profiles given below. All the views are in Beam's Eye View (BEV). G = Gun and T = Target.

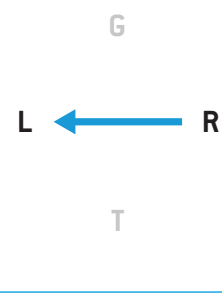
Beam commissioning limitations

Diagonal profiles (SCAN_DIAGONAL set to FIRST_DIAGONAL or SECOND_DIAGONAL) are only supported for photons. Diagonal profiles must cross the central axis. Only quadratic fields are supported for diagonal profiles. Only SCAN_ANGLE=0.00 is supported.

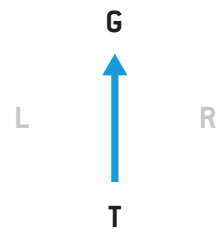
B.4.1 "Normal" Crossplane profile

Key name	Value	Illustration
CROSSPLANE_AXIS_DIR	LEFT_RIGHT	
SCAN_CURVETYPE	CROSSPLANE_PROFILE	
SCAN_ANGLE	0	
SCAN_DIAGONAL	NOT _DIAGONAL	

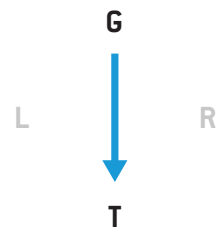
B.4.2 Crossplane profile at inverse direction definition of the LINAC

Key name	Value	Illustration
CROSSPLANE_AXIS_DIR	RIGHT_LEFT	
SCAN_CURVETYPE	CROSSPLANE_PROFILE	
SCAN_ANGLE	0	
SCAN_DIAGONAL	NOT _DIAGONAL	

B.4.3 "Normal" Inplane profile

Key name	Value	Illustration
INPLANE_AXIS_DIR	TARGET_GUN	
SCAN_CURVETYPE	INPLANE_PROFILE	
SCAN_ANGLE	0	
SCAN_DIAGONAL	NOT _DIAGONAL	

B.4.4 Inplane profile at inverse direction definition of the LINAC

Key name	Value	Illustration
INPLANE_AXIS_DIR	GUN_TARGET	
SCAN_CURVETYPE	INPLANE_PROFILE	
SCAN_ANGLE	0	
SCAN_DIAGONAL	NOT _DIAGONAL	

B.4.5 Diagonal profiles

In .mcc format, RayPhysics supports diagonal profiles where SCAN_DIAGONAL=FIRST_DIAGONAL or SCAN_DIAGONAL=SECOND_DIAGONAL. Only quadratic fields are supported. The keywords SCAN_DIAGONAL, SCAN_CURVETYPE and CROSSPLANE_AXIS_DIR/INPLANE_AXIS_DIR determine how the coordinates in the RayPhysics dose curve coordinate system are derived from the measuring positions in the dose curve file for a diagonal profile. The measuring positions are interpreted as radii positions and the x- and y-positions are calculated from the following equation.

$$x = y = \frac{radius}{\sqrt{2}} \qquad \text{[Eq. 18]}$$

The correct sign for the x- and y-positions is selected by taking the information from the keywords described above and converting to the dose curve coordinate system in RayPhysics.

The different directions that the measuring positions are stored in is shown by the arrow directions in the image below for the different combinations of SCAN_DIAGONAL, SCAN_CURVETYPE and CROSSPLANE_AXIS_DIR/INPLANE_AXIS_DIR. Note that CROSSPLANE_AXIS_DIR only is relevant for SCAN_CURVETYPE=CROSSPLANE_PROFILE and INPLANE_AXIS_DIR only is relevant for SCAN_CURVETYPE=INPLANE_PROFILE.

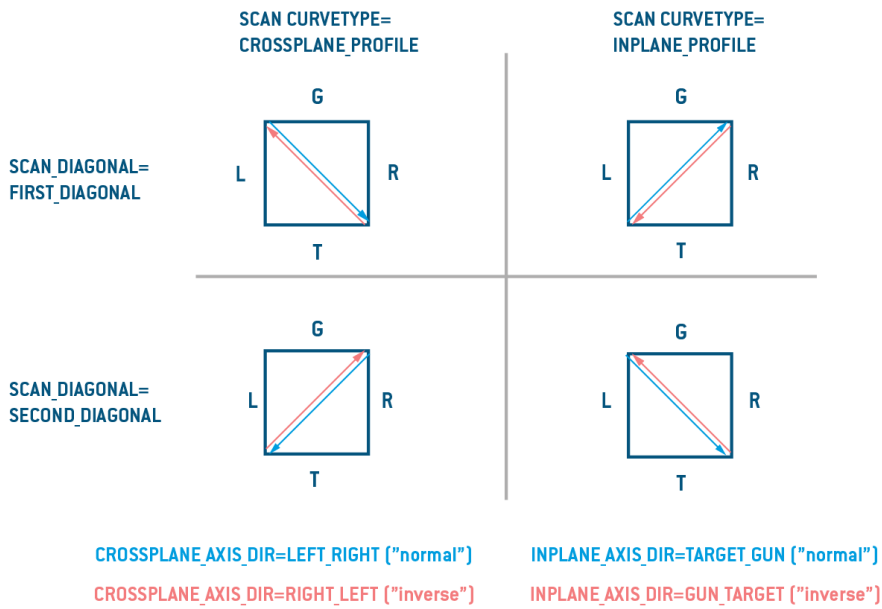


Figure 193. Diagonal profiles in mcc format

The table below contains an example of yielded x- and y-coordinates in the dose curve coordinate system in RayPhysics for a diagonal profile with:

SCAN_CURVETYPE=CROSSPLANE_PROFILE,

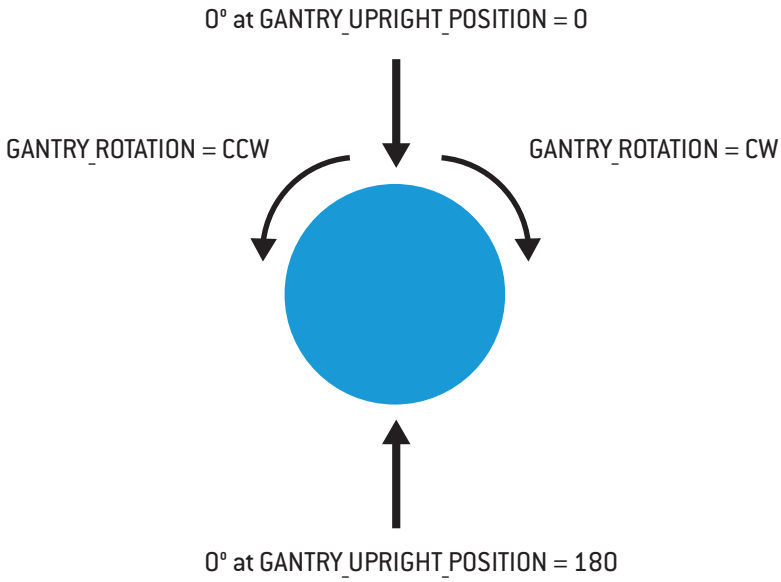
SCAN_DIAGONAL=FIRST_DIAGONAL,

CROSSPLANE_AXIS_DIR=LEFT_RIGHT.

Measuring position/radius	RayPhysics x-coordinate	RayPhysics y-coordinate
-10.0	-7.07	7.07
-5.0	-3.54	3.54
0.0	0.0	0.0
2.0	1.41	-1.41
4.0	2.83	-2.83
8.0	5.66	-5.66

B.4.6 Definition of the gantry in mcc

View from target to gun:



B.4.7 Example: electron dose curve

```
BEGIN_SCAN_DATA
FORMAT=CC-Export V1.80
FILE_CREATION_DATE=01-Jun-2005 15:22:00
LAST_MODIFIED=01-Jun-2005 15:22 BEGIN_SCAN 1
BEGIN_SCAN 1
MEAS_DATE=01-Jun-2005 15:22:00
LINAC=DEMO LINAC
COMMENT=After Service
MODALITY=EL
INPLANE_AXIS_DIR=GUN_TARGET
CROSSPLANE_AXIS_DIR=LEFT_RIGHT
ENERGY=4.00
SSD=1000.00
BLOCK=0
WEDGE=App10x10
FIELD_INPLANE=100.00
FIELD_CROSSPLANE=100.00
FIELD_TYPE=RECTANGULAR
GANTRY=0.00
GANTRY_UPRIGHT_POSITION=0
GANTRY_ROTATION=CW
COLL_ANGLE=0.00
SCAN_CURVETYPE=PDD
SCAN_DEPTH=0.00
SCAN_OFFAXIS_INPLANE=0.00
SCAN_OFFAXIS_CROSSPLANE=0.00
SCAN_ANGLE=0.00
SCAN_DIAGONAL=NOT_DIAGONAL
MEAS_UNIT=A.U.
BEGIN_DATA
0.00 1.4104E+00
1.50 1.5208E+00
3.00 1.5687E+00
4.50 1.5280E+00
6.00 1.4035E+00
7.50 1.1884E+00
9.00 950.04E-03
```

```
10.50 670.75E-03
12.00 412.93E-03
13.50 210.12E-03
15.00 76.585E-03
16.50 16.665E-03
18.00 5.3608E-03
19.50 4.2101E-03
21.00 4.1209E-03
22.50 3.8893E-03
24.00 3.8747E-03
25.50 3.8159E-03
27.00 3.7059E-03
28.50 3.7289E-03
30.00 3.6840E-03
32.50 3.5169E-03
35.00 3.3802E-03
37.50 3.3294E-03
40.00 3.1407E-03
45.00 2.9919E-03
50.00 2.8452E-03
END_DATA
END_SCAN 1
END_SCAN_DATA
```

B.4.8 Example: photon crossline profile with first diagonal

```
BEGIN_SCAN_DATA
FORMAT=CC-Export V1.9
FILE_CREATION_DATE=16-Apr-2015 21:04:24
LAST_MODIFIED=16-Apr-2015 21:04:24
BEGIN_SCAN 1
TASK_NAME=tba PDD Profiles
PROGRAM=tbaScan
COMMENT=QV6FFF_x_diagnonal_X40_Y40_SSD90_T100_W
MEAS_DATE=16-Apr-2015 20:54:50
LINAC=SYNERGY
MODALITY=X
ISOCENTER=1000.00
INPLANE_AXIS=Y
CROSSPLANE_AXIS=X
DEPTH_AXIS=Z
INPLANE_AXIS_DIR=GUN_TARGET
CROSSPLANE_AXIS_DIR=LEFT_RIGHT
DEPTH_AXIS_DIR=UP_DOWN
ENERGY=6.0
NOMINAL_DMAX=15.00
SSD=900.00
SCD=450.00
BLOCK=0
WEDGE_ANGLE=0.00
FIELD_INPLANE=400.00
FIELD_CROSSPLANE=400.00
FIELD_TYPE=RECTANGULAR
GANTRY=0.00
GANTRY_UPRIGHT_POSITION=0
GANTRY_ROTATION=CW
COLL_ANGLE=0.00
COLL_OFFSET_INPLANE=0.00
COLL_OFFSET_CROSSPLANE=0.00
SCAN_DEVICE=MP3
SCAN_DEVICE_SETUP=BARA_GUN_TARGET
ELECTROMETER=TANDEM
RANGE_FIELD=AUTO
```

```
RANGE_REFERENCE=AUTO
SCAN_CURVETYPE=CROSSPLANE_PROFILE
SCAN_DEPTH=100.00
SCAN_OFFAXIS_INPLANE=0.00
SCAN_OFFAXIS_CROSSPLANE=0.00
SCAN_ANGLE=0.00
SCAN_DIAGONAL=FIRST_DIAGONAL
SCAN_DIRECTION=POSITIVE
MEAS_MEDIUM=WATER
MEAS_UNIT=Gy/min
BEGIN_DATA
-9.90 17.785E+00
-8.49 17.779E+00
-7.07 17.791E+00
-5.66 17.815E+00
-4.24 17.875E+00
-2.83 17.899E+00
-1.41 17.875E+00
0.00 17.875E+00
1.41 17.893E+00
2.83 17.911E+00
4.24 17.899E+00
5.66 17.875E+00
7.07 17.869E+00
8.49 17.815E+00
9.90 17.797E+00
END_DATA
END_SCAN 1
END_SCAN_DATA
```

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